

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 29, 2002, 15:43:21 ; Search time 20.72 Seconds
(without alignments)
195.688 Million cell updates/sec

Title: SEQ2-49N-51T
 Perfect score: 875
 Sequence: 1 MSYNLLGFLQRSSNFQCKL.....RVEILRNFYFINRLTGYLRN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 sub

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Database : Issued_patents_AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query | | | DB | ID | Description |
|------------|-------|-------|--------|----|-------------------|--------------------|
| | Score | Match | Length | | | |
| 1 | 863 | 98.6 | 166 | 4 | US-09-397-992A-7 | Sequence 7, Appli |
| 2 | 863 | 98.6 | 166 | 6 | 5514567-4 | Patent No. 5514567 |
| 3 | 863 | 98.6 | 187 | 4 | US-09-206-903A-9 | Sequence 9, Appli |
| 4 | 863 | 98.6 | 187 | 4 | US-08-406-903A-30 | Sequence 30, Appli |
| 5 | 863 | 98.6 | 187 | 4 | US-09-202-122A-7 | Sequence 9, Appli |
| 6 | 863 | 98.6 | 187 | 4 | US-09-206-935-7 | Sequence 7, Appli |
| 7 | 863 | 98.6 | 187 | 4 | US-09-206-936-7 | Sequence 7, Appli |
| 8 | 863 | 98.6 | 187 | 6 | 5514567-1 | Patent No. 5514567 |
| 9 | 861 | 98.4 | 166 | 2 | US-08-477-310A-1 | Sequence 1, Appli |
| 10 | 858 | 98.1 | 166 | 1 | US-08-213-448-1 | Sequence 1, Appli |
| 11 | 858 | 98.1 | 166 | 3 | US-08-912-768-1 | Sequence 1, Appli |
| 12 | 858 | 98.1 | 166 | 5 | PCF-US95-03206-1 | Sequence 1, Appli |
| 13 | 858 | 98.1 | 187 | 3 | US-08-912-768-3 | Sequence 3, Appli |
| 14 | 855 | 97.7 | 187 | 1 | US-08-026-758-22 | Sequence 22, Appli |
| 15 | 846 | 96.7 | 187 | 6 | 5326859-1 | Patent No. 5326859 |
| 16 | 813 | 92.9 | 187 | 6 | 5510472-6 | Patent No. 5510472 |
| 17 | 803 | 91.8 | 166 | 1 | US-08-362-453-16 | Sequence 16, Appli |
| 18 | 561 | 64.1 | 187 | 1 | US-08-026-758-21 | Sequence 21, Appli |
| 19 | 481.5 | 55.0 | 186 | 1 | US-08-026-758-25 | Sequence 25, Appli |
| 20 | 451.5 | 51.6 | 186 | 1 | US-08-026-758-26 | Sequence 26, Appli |
| 21 | 429.5 | 49.1 | 186 | 1 | US-08-026-758-24 | Sequence 24, Appli |
| 22 | 363.5 | 41.5 | 186 | 1 | US-08-026-758-23 | Sequence 23, Appli |
| 23 | 257.5 | 29.4 | 208 | 4 | US-09-397-992A-5 | Sequence 5, Appli |
| 24 | 253.5 | 29.0 | 192 | 4 | US-09-397-992A-27 | Sequence 27, Appli |
| 25 | 253.5 | 29.0 | 193 | 4 | US-09-397-992A-26 | Sequence 26, Appli |
| 26 | 253.5 | 29.0 | 193 | 4 | US-09-397-992A-29 | Sequence 29, Appli |
| 27 | 253.5 | 29.0 | 208 | 4 | US-09-206-903A-1 | Sequence 1, Appli |

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| 28 | 253.5 | 29.0 | 208 | 4 | US-09-202-122-1 | Sequence 1, Appl1 |
| 29 | 253.5 | 29.0 | 208 | 4 | US-09-206-935-1 | Sequence 1, Appl1 |
| 30 | 253.5 | 29.0 | 208 | 4 | US-09-397-994A-2 | Sequence 13, Appl1 |
| 31 | 252 | 28.1 | 166 | 3 | US-08-819-238A-13 | Sequence 86, Appl1 |
| 32 | 249.5 | 28.5 | 166 | 4 | US-09-339-913B-86 | Sequence 86, Appl1 |
| 33 | 249.5 | 28.5 | 166 | 4 | US-09-339-904A-86 | Sequence 86, Appl1 |
| 34 | 249.5 | 28.5 | 166 | 4 | US-08-769-063B-86 | Sequence 86, Appl1 |
| 35 | 249.5 | 28.5 | 166 | 4 | US-09-344-003B-86 | Sequence 86, Appl1 |
| 36 | 249.5 | 28.5 | 189 | 4 | US-09-206-935-17 | Sequence 17, Appl1 |
| 37 | 249.5 | 28.5 | 189 | 4 | US-08-706-936-17 | Sequence 17, Appl1 |
| 38 | 249 | 28.5 | 166 | 3 | US-08-819-238A-1 | Sequence 1, Appl1 |
| 39 | 247 | 28.2 | 166 | 2 | US-08-631-328-55 | Sequence 55, Appl1 |
| 40 | 245.5 | 28.1 | 168 | 1 | US-08-249-671A-5 | Sequence 5, Appl1 |
| 41 | 245.5 | 28.1 | 185 | 1 | US-08-249-671A-5 | Sequence 11, Appl1 |
| 42 | 244.5 | 27.9 | 165 | 1 | US-08-024-330-1 | Sequence 1, Appl1 |
| 43 | 244.5 | 27.9 | 165 | 1 | US-07-952-840-1 | Sequence 1, Appl1 |
| 44 | 244.5 | 27.9 | 165 | 1 | US-08-356-021-1 | Sequence 1, Appl1 |
| 45 | 244.5 | 27.9 | 165 | 5 | PCR-US94-01739-1 | Sequence 1, Appl1 |

ALIGNMENTS

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RESULT 1
US-09-397-992A-7
; Sequence 7, Application US/09397992A
; Patent No. 6329175
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell
; APPLICANT: Grant, Francis J.
; APPLICANT: Rixon, Mark W.
; APPLICANT: Kindsvoegel, Wayne
; TITLE OF INVENTION: Interferon-epsilon
; FILE REFERENCE: 98-46
; CURRENT APPLICATION NUMBER: US/09/397,992A
; CURRENT FILING DATE: 1999-09-16
; PRIOR APPLICATION NUMBER: 60/101,012
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/118,578
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/142,766
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-992A-7

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[illegible]

RESULT 2
5514567-4
; Patent No. 5514567
; APPLICANT: SUGANO, HARUO; MURAMATSU, MASAMI; TANIGUCHI,
; TADATSUGU

; TITLE OF INVENTION: DNA AND RECOMBINANT PLASMID
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,179
; FILING DATE: 06-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 389,922
; FILING DATE: 18-JUN-1982
; APPLICATION NUMBER: 201,359
; FILING DATE: 27-OCT-1980
; SEQ ID NO:4:
; LENGTH: 166
; 5514567-4

Query Match 98.68; Score 863; DB 6; Length 166;
Best Local Similarity 98.8; Pred. No. 7.3e-83;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQSSNFQCKLLQWLNGLRLEYCLKDRMNFDPPEIKQLQNFCKEDAALTYI 60
DB 1 MSYNLLGFLQSSNFQCKLLQWLNGLRLEYCLKDRMNFDPPEIKQLQNFCKEDAALTYI 60

QY 61 EMLQNIFAIRQDSSSTGNETIVENLLANYHQNHLKTVLEEKLEKEDFTRGKLMSL 120
DB 61 EMLQNIFAIRQDSSSTGNETIVENLLANYHQNHLKTVLEEKLEKEDFTRGKLMSL 120

QY 121 HLKRYGRILHYLKAKEYSHCAWTVRVEILRNFYFINRLTYGLRN 166
DB 121 HLKRYGRILHYLKAKEYSHCAWTVRVEILRNFYFINRLTYGLRN 166

RESULT 3
US-09-206-903A-9
; Sequence 9, Application US/09206903A
; Patent No. 6200780
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Godowski, Paul J.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Dong-Xiao
; TITLE OF INVENTION: NOVEL TYPE I INTERFERONS
; FILE REFERENCE: P1224-2R1
; CURRENT APPLICATION NUMBER: US/09/206,903A
; CURRENT FILING DATE: 1998-12-07
; PRIOR APPLICATION NUMBER: US 60/106,463
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-206-903A-9

Query Match 98.68; Score 863; DB 4; Length 187;
Best Local Similarity 98.8; Pred. No. 8.5e-83;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQSSNFQCKLLQWLNGLRLEYCLKDRMNFDPPEIKQLQNFCKEDAALTYI 60
DB 22 MSYNLLGFLQSSNFQCKLLQWLNGLRLEYCLKDRMNFDPPEIKQLQNFCKEDAALTYI 81

QY 61 EMLQNIFAIRQDSSSTGNETIVENLLANYHQNHLKTVLEEKLEKEDFTRGKLMSL 120
DB 82 EMLQNIFAIRQDSSSTGNETIVENLLANYHQNHLKTVLEEKLEKEDFTRGKLMSL 141

QY 121 HLKRYGRILHYLKAKEYSHCAWTVRVEILRNFYFINRLTYGLRN 166
DB 142 HLKRYGRILHYLKAKEYSHCAWTVRVEILRNFYFINRLTYGLRN 187

RESULT 4

US-08-406-030A-30
; Sequence 30, Application US/08406030A
; Patent No. 6270989
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Hauge, Brian M.
; APPLICANT: Selden, Richard F.
; TITLE OF INVENTION: Protein Production and Delivery
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.c.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,030A
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/243,391
; FILING DATE: 13-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,586
; FILING DATE: 03-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,533
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,840
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,188
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11704
; FILING DATE: 02-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09627
; FILING DATE: 05-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: TKT95-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-406-030A-30

Query Match 98.6%; Score 863; DB 4; Length 187;
Best Local Similarity 98.8%; Pred. No. 8.5e-83;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQSSNFQCKLLQWLNGLRLEYCLKDRMNFDPPEIKQLQNFCKEDAALTYI 60
DB 22 MSYNLLGFLQSSNFQCKLLQWLNGLRLEYCLKDRMNFDPPEIKQLQNFCKEDAALTYI 81

QY 61 EMLQNIFAIRQDSSSTGNETIVENLLANYHQNHLKTVLEEKLEKEDFTRGKLMSL 120

Db 82 EMLQNIFAIFRODSSSTGNETIVENLLANVYHQINHLKTVLEKLEKEDFTRGKLMSSL 141
Qy 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
Db 142 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 187

RESULT 5
US-09-202-122-9
; Sequence 9, Application US/09202122
; Patent No. 6299869
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Godowski, Paul
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Dong-Xiao
; TITLE OF INVENTION: HUMAN INTERFERON-EPSILON: A TYPE I INTERFERON
; FILE REFERENCE: P1224R2 (filed)
; CURRENT APPLICATION NUMBER: US/09/202,122
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: PCT/US98/25672
; PRIOR FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 9
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-202-122-9

Query Match 98.6%; Score 863; DB 4; Length 187;
Best Local Similarity 98.8%; Pred. No. 8.5e-83;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 22 MSYNLLGFLQSSNFQCKLLWQLNGRLEYCLKDRNFDPPEIKQLQNFKEDAAALTYI 81
Qy 61 EMLQNIFAIFRODSSSTGNETIVENLLANVYHQINHLKTVLEKLEKEDFTRGKLMSSL 120
Db 82 EMLQNIFAIFRODSSSTGNETIVENLLANVYHQINHLKTVLEKLEKEDFTRGKLMSSL 141
Qy 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
Db 142 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 187

RESULT 6
US-09-206-935-7
; Sequence 7, Application US/09206935
; Patent No. 6299877
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Godowski, Paul
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Dong-Xiao
; TITLE OF INVENTION: NOVEL TYPE I INTERFERONS
; FILE REFERENCE: 11669.50US05
; CURRENT APPLICATION NUMBER: US/09/206,935
; CURRENT FILING DATE: 1998-12-07
; EARLIER APPLICATION NUMBER: 60/084,045
; EARLIER FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-206-935-7

Query Match 98.6%; Score 863; DB 4; Length 187;
Best Local Similarity 98.8%; Pred. No. 8.5e-83;

Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MSYNLLGFLQSSNFQCKLLWQLNGRLEYCLKDRNFDPPEIKQLQNFKEDAAALTYI 60
Db 22 MSYNLLGFLQSSNFQCKLLWQLNGRLEYCLKDRNFDPPEIKQLQNFKEDAAALTYI 81
Qy 61 EMLQNIFAIFRODSSSTGNETIVENLLANVYHQINHLKTVLEKLEKEDFTRGKLMSSL 120
Db 82 EMLQNIFAIFRODSSSTGNETIVENLLANVYHQINHLKTVLEKLEKEDFTRGKLMSSL 141
Qy 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
Db 142 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 187

RESULT 7
US-09-206-936-7
; Sequence 7, Application US/09206936A
; Patent No. 6300475
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: No. 6300475el Inteferon
; FILE REFERENCE: P1224R1
; CURRENT APPLICATION NUMBER: US/09/206,936A
; CURRENT FILING DATE: 1998-12-07
; EARLIER APPLICATION NUMBER: US 60/067,897
; EARLIER FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 7
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-206-936-7

Query Match 98.6%; Score 863; DB 4; Length 187;
Best Local Similarity 98.8%; Pred. No. 8.5e-83;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MSYNLLGFLQSSNFQCKLLWQLNGRLEYCLKDRNFDPPEIKQLQNFKEDAAALTYI 60
Db 22 MSYNLLGFLQSSNFQCKLLWQLNGRLEYCLKDRNFDPPEIKQLQNFKEDAAALTYI 81
Qy 61 EMLQNIFAIFRODSSSTGNETIVENLLANVYHQINHLKTVLEKLEKEDFTRGKLMSSL 120
Db 82 EMLQNIFAIFRODSSSTGNETIVENLLANVYHQINHLKTVLEKLEKEDFTRGKLMSSL 141
Qy 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
Db 142 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 187

RESULT 8
5514567-1
; Patent No. 5514567
; APPLICANT: SUGANO, HARUO; MURAMATSU, MASAMI; TANIGUCHI, TADATSUGU
; TITLE OF INVENTION: DNA AND RECOMBINANT PLASMID
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,179
; FILING DATE: 06-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 389,922
; FILING DATE: 18-JUN-1982
; APPLICATION NUMBER: 201,359
; FILING DATE: 27-OCT-1980
; SEQ ID NO:1:
; LENGTH: 187
5514567-1

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Query Match          98.6%; Score 863; DB 6; Length 187;
Best Local Similarity 98.8%; Pred. No. 8.5e-83;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQSSNFQCKLLWOLNGRLEYCLKDRNFDIPEEIKQLQNFtKEDAAALTYI 60
DB 22 MSYNLLGFLQSSNFQCKLLWOLNGRLEYCLKDRNFDIPEEIKQLQNFQKEDAAALTYI 81
QY 61 EMLQNIFAIFRODSSSTGNETIVENLLANYHQLNHLKTIVLEEKLEKEDFTRGKLMSSL 120
DB 82 EMLQNIFAIFRODSSSTGNETIVENLLANYHQLNHLKTIVLEEKLEKEDFTRGKLMSSL 141
QY 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLRN 166
DB 142 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLRN 187

RESULT 9
US-08-477-310A-1
; Sequence 1, Application US/08477310A
; Patent No. 5814485
; GENERAL INFORMATION:
; APPLICANT: Dorin, Glenn
; APPLICANT: McAlary, Patrick J.
; APPLICANT: Wong, Kathleen M.
; TITLE OF INVENTION: Bacterial Production of Hydrophobic
; TITLE OF INVENTION: Polypeptides
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,310A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chung, Ling-Fong
; REGISTRATION NUMBER: 36,482
; REFERENCE/DOCKET NUMBER: 960,001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2704
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-310A-1

Query Match          98.4%; Score 861; DB 2; Length 166;
Best Local Similarity 98.2%; Pred. NO. 1.2e-82;
Matches 163; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQSSNFQCKLLWOLNGRLEYCLKDRNFDIPEEIKQLQNFtKEDAAALTYI 60
DB 1 MSYNLLGFLQSSNFQCKLLWOLNGRLEYCLKDRNFDIPEEIKQLQNFQKEDAAALTYI 60
QY 61 EMLQNIFAIFRODSSSTGNETIVENLLANYHQLNHLKTIVLEEKLEKEDFTRGKLMSSL 120
DB 61 EMLQNIFAIFRODSSSTGNETIVENLLANYHQLNHLKTIVLEEKLEKEDFTRGKLMSSL 120

Query Match          98.1%; Score 858; DB 1; Length 166;
Best Local Similarity 98.2%; Pred. No. 2.4e-82;
Matches 163; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 1 MSYNLLGFLQSSNFQCKLLWOLNGRLEYCLKDRNFDIPEEIKQLQNFQKEDAAALTYI 60
QY 61 EMLQNIFAIFRODSSSTGNETIVENLLANYHQLNHLKTIVLEEKLEKEDFTRGKLMSSL 120
DB 61 EMLQNIFAIFRODSSSTGNETIVENLLANYHQLNHLKTIVLEEKLEKEDFTRGKLMSSL 120
QY 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLRN 166
DB 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLRN 166

RESULT 11
US-08-912-768-1
; Sequence 1, Application US/08912768
; Patent No. 6127332
; GENERAL INFORMATION:
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QY 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLRN 166
DB 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLRN 166

RESULT 10
US-08-213-448-1
; Sequence 1, Application US/08213448
; Patent No. 5545723
; GENERAL INFORMATION:
; APPLICANT: Goelz, Susan E
; APPLICANT: Cate, Richard L
; APPLICANT: Pepinsky, Blake R
; APPLICANT: Chow, Pingchang E
; TITLE OF INVENTION: No. 5545723el Muteins Of IFN-Beta
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr.
; STREET: Fish & Neave, 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/213,448
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-213-448-1

Query Match          98.1%; Score 858; DB 1; Length 166;
Best Local Similarity 98.2%; Pred. No. 2.4e-82;
Matches 163; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQSSNFQCKLLWOLNGRLEYCLKDRNFDIPEEIKQLQNFtKEDAAALTYI 60
DB 1 MSYNLLGFLQSSNFQCKLLWOLNGRLEYCLKDRNFDIPEEIKQLQNFQKEDAAALTYI 60
QY 61 EMLQNIFAIFRODSSSTGNETIVENLLANYHQLNHLKTIVLEEKLEKEDFTRGKLMSSL 120
DB 61 EMLQNIFAIFRODSSSTGNETIVENLLANYHQLNHLKTIVLEEKLEKEDFTRGKLMSSL 120
QY 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLRN 166
DB 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLRN 166

RESULT 11
US-08-912-768-1
; Sequence 1, Application US/08912768
; Patent No. 6127332
; GENERAL INFORMATION:
```

```
; APPLICANT: Goelz, Susan E
; APPLICANT: Cate, Richard L
; APPLICANT: Pepinsky, Blake R
; APPLICANT: Chow, Pingchang E
; TITLE OF INVENTION: No. 6127332el Muteins Of IFN-Beta
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr.
; STREET: Fish & Neave, 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,768
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/475,774
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PCT-US95-03206-1

Query Match 98.1%; Score 858; DB 3; Length 166;
Best Local Similarity 98.2%; Pred. No. 2.4e-82;
Matches 163; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSYNLLGFLQRSSNFQCKLLQNLNGLRLEYCLKDRMNFDPPEIKQLQNFKEDAAITY 60
Db 1 MSYNLLGFLQRSSNFQCKLLQNLNGLRLEYCLKDRMNFDPPEIKQLQNFKEDAAITY 60

Qy 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
Db 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120

Qy 121 HLKRYGRILHLKAKESYSHCAWTVRVEILRNFFYNRLTGYLRN 166
Db 121 HLKRYGRILHLKAKESYSHCAWTVRVEILRNFFYNRLTGYLRN 166

RESULT 12
PCT-US95-03206-1
; Sequence 1, Application PC/TUS9503206
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Goelz, Susan E
; APPLICANT: Cate, Richard L
; APPLICANT: Pepinsky, Blake R
; APPLICANT: Chow, Pingchang E
; TITLE OF INVENTION: Novel Muteins Of IFN-Beta
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: James F. Haley, Jr.
; STREET: Fish & Neave, 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03206
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PCT-US95-03206-1

Query Match 98.1%; Score 858; DB 5; Length 166;
Best Local Similarity 98.2%; Pred. No. 2.4e-82;
Matches 163; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSYNLLGFLQRSSNFQCKLLQNLNGLRLEYCLKDRMNFDPPEIKQLQNFKEDAAITY 60
Db 1 MSYNLLGFLQRSSNFQCKLLQNLNGLRLEYCLKDRMNFDPPEIKQLQNFKEDAAITY 60

Qy 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
Db 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120

Qy 121 HLKRYGRILHLKAKESYSHCAWTVRVEILRNFFYNRLTGYLRN 166
Db 121 HLKRYGRILHLKAKESYSHCAWTVRVEILRNFFYNRLTGYLRN 166

RESULT 13
US-08-912-768-3
; Sequence 3, Application US/08912768
; Patent No. 6127332
; GENERAL INFORMATION:
; APPLICANT: Goelz, Susan E
; APPLICANT: Cate, Richard L
; APPLICANT: Pepinsky, Blake R
; APPLICANT: Chow, Pingchang E
; TITLE OF INVENTION: No. 6127332el Muteins Of IFN-Beta
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr.
; STREET: Fish & Neave, 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,768
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,774
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-768-3

Query Match 98.1%; Score 858; DB 3; Length 187;
Best Local Similarity 98.2%; Pred. No. 2.8e-82;
Matches 163; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MSYNLLGFLQRSSNFQCKLLQWLNGLRLEYCLKDRMNFDPPEIKQLQKFCKEDAALTY 60
Db 22 MSYNLLGFLQRSSNFQCKLLQWLNGLRLEYCLKDRMNFDPPEIKQLQKFCKEDAALTY 81
Qy 61 EMLQNIFAIFRODSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
Db 82 EMLQNIFAIFRODSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSL 141
Qy 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
Db 142 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 187

RESULT 14
US-08-026-758-22
Sequence 22, Application US/08026758
Patent No. 5780021
GENERAL INFORMATION:
APPLICANT: SOBEL, DOUGLAS O.
TITLE OF INVENTION: A METHOD FOR TREATING AUTOIMMUNE
TITLE OF INVENTION: DISEASES USING ALPHA-INTERFERON AND/OR BETA-INTERFERON
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/026,758
FILING DATE: 19930305
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5780021man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-096-0
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 22..187
OTHER INFORMATION: /note- "Hu-IFN-beta"
US-08-026-758-22

Query Match 97.7%; Score 855; DB 1; Length 187;
Best Local Similarity 98.2%; Pred. No. 5.9e-82;
Matches 163; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MSYNLLGFLQRSSNFQCKLLQWLNGLRLEYCLKDRMNFDPPEIKQLQKFCKEDAALTY 60
Db 22 MSYNLLGFLQRSSNFQCKLLQWLNGLRLEYCLKDRMNFDPPEIKQLQKFCKEDAALTY 81
Qy 61 EMLQNIFAIFRODSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
Db 82 EMLQNIFAIFRODSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSL 141
Qy 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
Db 142 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 187
RESULT 15
5326859-1
Patent No. 5326859
APPLICANT: Sugano, Haruo; Muramatsu, Masami; Taniguchi, Tadatsugu
TITLE OF INVENTION: DNA AND RECOMBINANT PLASMID
NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/201,359
FILING DATE: 27-OCT-1980
SEQ ID NO: 1:
LENGTH: 187
5326859-1

Query Match 96.7%; Score 846; DB 6; Length 187;
Best Local Similarity 97.0%; Pred. No. 5.1e-81;
Matches 161; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MSYNLLGFLQRSSNFQCKLLQWLNGLRLEYCLKDRMNFDPPEIKQLQKFCKEDAALTY 60
Db 22 MSYNLLGFLQRSSNFQCKLLQWLNGLRLEYCLKDRMNFDPPEIKQLQKFCKEDAALTY 81
Qy 61 EMLQNIFAIFRODSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
Db 82 EMLQNIFAIFRODSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSL 141
Qy 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
Db 142 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 187

Search completed: July 29, 2002, 15:43:22
Job time: 223 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 29, 2002, 15:39:04 ; Search time 51.64 Seconds
(without alignments)
357.054 Million cell updates/sec

Title: SEQ2-49N-51S
Perfect score: 874
Sequence: 1 MSYNLGFLQRSSNFQCKL.....RVELRNFYFINKLTGYLRN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
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4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
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11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
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13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
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15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
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18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
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22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-----------------------------|
| 1 | 870 | 99.5 | 166 | 22 | AAU00119 Human interferon b |
| 2 | 864 | 98.9 | 166 | 4 | AAP30219 Sequence of interf |
| 3 | 864 | 98.9 | 166 | 6 | AAP50262 Sequence encoded b |
| 4 | 864 | 98.9 | 166 | 6 | AAP50279 Protein sequence e |
| 5 | 864 | 98.9 | 166 | 7 | AA1984 Oxidation resistan |
| 6 | 864 | 98.9 | 166 | 8 | AA1985 Sequence of interf |
| 7 | 864 | 98.9 | 166 | 19 | AA1986 Human native inter |
| 8 | 864 | 98.9 | 166 | 22 | AAE10346 Mature human beta- |
| 9 | 864 | 98.9 | 166 | 22 | AAE11979 Human wild-type in |
| 10 | 864 | 98.9 | 166 | 22 | AAU00038 Human interferon b |
| 11 | 864 | 98.9 | 166 | 22 | AAU00074 Human interferon b |

| | | | | | |
|----|-----|------|-----|----|-----------------------------|
| 12 | 864 | 98.9 | 166 | 22 | AA19356 Human INF-beta A-c |
| 13 | 864 | 98.9 | 166 | 22 | AA19357 Human INF-beta B-c |
| 14 | 864 | 98.9 | 177 | 6 | AAP50261 Sequence of beta-i |
| 15 | 864 | 98.9 | 183 | 21 | AA194920 Amino acid sequenc |
| 16 | 864 | 98.9 | 183 | 21 | AA194920 Histidine tagged-h |
| 17 | 864 | 98.9 | 187 | 2 | AAP10016 Sequence of fibrob |
| 18 | 864 | 98.9 | 187 | 3 | AAP20026 Human fibroblast i |
| 19 | 864 | 98.9 | 187 | 15 | AA195987 Human fibroblast i |
| 20 | 864 | 98.9 | 187 | 19 | AA195987 Human interferon b |
| 21 | 864 | 98.9 | 187 | 20 | AA195987 Human HCMV inducib |
| 22 | 864 | 98.9 | 187 | 22 | AA195987 Human beta-interfe |
| 23 | 864 | 98.9 | 187 | 22 | AA195987 Human interferon b |
| 24 | 864 | 98.9 | 399 | 21 | AA195987 Human interferon-b |
| 25 | 864 | 98.9 | 415 | 20 | AA195987 IFNAR2/IFN-beta co |
| 26 | 864 | 98.9 | 166 | 7 | AAP60687 Sequence between t |
| 27 | 862 | 98.6 | 166 | 22 | AAU00103 Human interferon b |
| 28 | 862 | 98.6 | 166 | 22 | AAU00150 Human interferon b |
| 29 | 861 | 98.5 | 166 | 22 | AAU00070 Human interferon b |
| 30 | 861 | 98.5 | 166 | 22 | AAU00072 Human interferon b |
| 31 | 861 | 98.5 | 166 | 22 | AAU00075 Human interferon b |
| 32 | 861 | 98.5 | 166 | 22 | AAU00083 Human interferon b |
| 33 | 861 | 98.5 | 166 | 22 | AAU00085 Human interferon b |
| 34 | 861 | 98.5 | 166 | 22 | AAU00124 Human interferon b |
| 35 | 861 | 98.5 | 166 | 22 | AAU00143 Human interferon b |
| 36 | 861 | 98.5 | 166 | 22 | AAU00159 Human interferon b |
| 37 | 861 | 98.5 | 166 | 22 | AAU00160 Human interferon b |
| 38 | 861 | 98.5 | 187 | 3 | AAP20049 Interferon-beta ge |
| 39 | 860 | 98.4 | 166 | 22 | AAU00073 Human interferon b |
| 40 | 860 | 98.4 | 166 | 22 | AAU00077 Human interferon b |
| 41 | 860 | 98.4 | 166 | 22 | AAU00078 Human interferon b |
| 42 | 859 | 98.3 | 165 | 22 | AAU00139 Human interferon b |
| 43 | 859 | 98.3 | 166 | 6 | AAP50197 Modified human int |
| 44 | 859 | 98.3 | 166 | 16 | AA1982607 IFN-beta(Phel01). |
| 45 | 859 | 98.3 | 166 | 22 | AAU00079 Human interferon b |

ALIGNMENTS

| | |
|----------|--|
| RESULT 1 | |
| AAU00119 | |
| ID | AAU00119 standard; Protein; 166 AA. |
| XX | |
| AC | AAU00119; |
| XX | |
| DT | 16-MAY-2001 (first entry) |
| XX | |
| DE | Human Interferon beta mutant Q49N/Q51T. |
| XX | |
| KW | Human; interferon beta; antibody; multiple sclerosis; gene therapy; |
| KW | viral infection; viral hepatitis; cancer; breast cancer; inflammation; |
| KW | Crohn's disease; acute myeloid leukaemia; Hodgkin's disease; |
| KW | ulcerative colitis; immunomodulation; mutant; mutein; Q49N/Q51T. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| EH | Key |
| FT | Location/Qualifiers |
| FT | Misc-difference 49 /note= "Wild-type Gln replaced with Asn" |
| FT | Misc-difference 51 /note= "Wild-type Gln replaced with Thr" |
| XX | |
| PN | WO200115736-A2. |
| XX | |
| PD | 08-MAR-2001. |
| XX | |
| PF | 25-AUG-2000; 2000WO-DK00471. |
| XX | |
| PR | 27-AUG-1999; 99DK-0001197. |
| PR | 21-OCT-1999; 99US-0160782. |
| PR | 26-NOV-1999; 99DK-0001691. |
| PR | 07-FEB-2000; 2000DK-0000194. |
| PR | 07-MAR-2000; 2000DK-0000363. |

PR 14-APR-2000; 2000DK-0000642.
 PA (MAXY-) MAXYGEN APS.
 XX Pedersen AH, Schambye HT, Andersen KV, Bornaes C, Rasmussen PB;
 PI WPI; 2001-218488/22.
 XX
 XX
 XX A conjugate exhibiting interferon beta activity useful for treating
 PT multiple sclerosis comprises a non-polypeptide group covalently
 PT attached to an interferon beta polypeptide -
 XX
 XX Claim 39; Page - ; 108pp; English.
 XX
 CC The sequence represents Human interferon beta mutant Q49N/Q51T.
 CC Conjugates of the invention exhibiting interferon beta activity
 CC comprise at least one first non-polypeptide group covalently attached
 CC to an interferon beta polypeptide, the amino acid sequence of which
 CC differs from wild-type human interferon beta in at least one introduced
 CC and at least one removed amino acid residue comprising an attachment
 CC group for the first non-polypeptide group. The invention also concerns
 CC reducing the immunogenicity and/or increasing functional in vivo
 CC half-life and/or serum half-life of an interferon beta polypeptide
 CC comprising introducing an amino acid residue constituting an attachment
 CC group for a first non-polypeptide group into a position exposed at the
 CC surface of the protein that does not contain such a group and removing
 CC an amino acid residue constituting an attachment group for a first
 CC non-polypeptide group and subjecting the modified peptide to conjugation
 CC with the non-polypeptide group. The conjugate and a cell culture
 CC expressing the mutated polypeptides are useful in the treatment of
 CC disease, especially multiple sclerosis, and for treating mammals having
 CC circulating antibodies against interferon beta la or lb. DNA encoding the
 CC mutated proteins may be used for gene therapy. The DNA and proteins can
 CC also be used to treat viral infections (e.g. viral hepatitis), cancer
 CC (e.g. breast cancer), inflammation, Crohn's disease, acute myeloid
 CC leukaemia, Hodgkin's disease and ulcerative colitis and for
 CC immunomodulation.
 CC Note: the present sequence is not shown in the specification but is
 CC derived from the human interferon beta sequence given in AAU000038.
 XX
 SQ Sequence 166 AA;

Query Match 99.5%; Score 870; DB 22; Length 166;
 Best Local Similarity 99.4%; Pred. No. 4.4e-68;
 Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSYNLLGLQRSSNFQCKLLWQLNGRLCYCLKDRMNFDPPEIKQLQNFsKEDAALTY 60
 |||||
 Db 1 msynllglqrssnfqckllwqlngrieyclckdrmmfdipeelkqlqnfqkedaaltiy 60
 QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSL 120
 |||||
 Db 61 emlqnifaifrqdsstgwnetivenllanvyhqinhktvleeklekedftrgklmsl 120
 QY 121 HLKRYGRIILHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLRLN 166
 |||||
 Db 121 hlkrvgriilhyllkakeyshcawtivrveilrnfynrltgyrln 166

RESULT 2

AAP30219
 ID AAP30219 standard; Protein; 166 AA.

XX
 AC AAP30219;

XX 25-MAY-1992 (first entry)

XX Sequence of interferon (HuIFN) -beta-1 encoded by plasmid
 DE pDM101/trp/beta-1.

XX Hybrid interferon; antiviral; therapy; cancer; tumour.

OS Homo sapiens.

XX W08302461-A.

XX 21-JUL-1983.

XX 18-JAN-1983; 83WO-0900607.

XX 19-JAN-1982; 82US-0340782.

PR 03-FEB-1983; 83US-0463574.

PR 15-JUL-1985; 85US-0755265.

XX (CETU-) CETUS CORP.

XX Mark DF, Creasey AA;

XX WPI; 1983-723186/30.

XX N-PSDB; AAN30152.

XX Multi-class hybrid interferon poly-peptide(s) - with restricted
 PT antiviral and cell growth regulatory activities

XX Example; Fig 5; 61pp; English.

CC The inventors claim a multiclass hybrid interferon polypeptide and a
 CC DNA unit having a nucleotide sequence which encodes it. Pref. the
 CC AA sequence consists of alpha and beta interferons. Pref. IF1 is
 CC (i) the 1-73 AA seq. of HuIFN-alpha-1 (and IF2 is the 74-166 AA seq.
 CC of HuIFN-beta-1) (see AAN30155, AAP30222); or (ii) the 1-41 AA seq. of
 CC HuIFN-alpha-61A (and IF2 is the 43-166 AA seq. of HuIFN-beta-1) (see
 CC AAN30160, AAP30227). Alternatively IF1 is the amino terminal end of a
 CC beta-IF and IF2 is the carboxy terminal of an alpha-IF (esp. the
 CC 1-73 seq. of HuIFN-beta-1 and the 74-167 seq. of HuIFN-alpha-1
 CC resp.) (see AAN30156, AAP30223). In the examples plasmids pGW5 and
 CC pDM101/trp/beta-1 and p-alpha-61A were used (see AAN30151, AAN30152,
 CC AAN30157). HinfI was used to digest the DNA sequences in the region
 CC of significant handicaps (see AAN30153, AAN30154, AAN30158, AAN30159),
 CC and the restriction fragments were ligated to form hybrid DNA.

XX Sequence 166 AA;

Query Match 98.9%; Score 864; DB 4; Length 166;

Best Local Similarity 98.8%; Pred. No. 1.5e-67;

Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGLQRSSNFQCKLLWQLNGRLCYCLKDRMNFDPPEIKQLQNFsKEDAALTY 60
 |||||

Db 1 msynllglqrssnfqckllwqlngrieyclckdrmmfdipeelkqlqnfqkedaaltiy 60
 |||||

QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSL 120
 |||||

Db 61 emlqnifaifrqdsstgwnetivenllanvyhqinhktvleeklekedftrgklmsl 120
 |||||

QY 121 HLKRYGRIILHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLRLN 166
 |||||

Db 121 hlkrvgriilhyllkakeyshcawtivrveilrnfynrltgyrln 166
 |||||

RESULT 3

AAP30262

ID AAP50262 standard; Protein; 166 AA.

XX
 AC AAP50262;

XX 20-NOV-1991 (first entry)

XX Sequence encoded by the sequence between the EcoRI site and the
 DE XhoII site of p-beta-1-trp.

XX Expression vector; trp promoter-operator; transformed bacteria.

XX US4499188-A.


```
XX PD 12-FEB-1985.
XX XX
XX PF 05-MAY-1982; 82US-0375098.
XX XX
XX PR 05-MAY-1982; 82US-0375098.
XX PR 23-JAN-1984; 84CA-0445883.
XX XX
XX PA (CETU-) CETUS CORP.
XX PA (CETU ) CETUS CORP.
XX XX
XX PI Konrad MW, Mark DF;
XX XX
XX DR WPI; 1985-055962/09.
XX DR N-PSDB; AAN50289.
XX XX
XX PT Polypeptide, esp. interferon, prodn. by transformed bacteria -
XX PT cultured in presence of a repressor which is consumed during
XX PT growth
XX XX
XX PS Example; Fig 5; 12pp; English.
XX PS
XX CC The inventors claim a process for the prodn. of heterologous
XX CC polypeptide by transformed bacteria. The pref. promoter-operator is
XX CC trp which controls expression of structural genes encoding
XX CC polypeptides of a synthetic pathway forming tryptophan, esp. at a
XX CC concn. of 5.3T mg/l (T= predetermined turbidity value measured at
XX CC 680nm, esp. 10-100). The transformed bacteria are esp. E.coli contg.
XX CC the plasmid p-beta-1-trp. Example 1 concerns the construction of
XX CC plasmid p-beta-1-trp for the direct expression of IFN-beta under the
XX CC control of trp promoter-operator.
XX XX
XX SQ Sequence 166 AA;

Query Match 98.9%; Score 864; DB 6; Length 166;
Best Local Similarity 98.8%; Pred. No. 1.5e-67;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSYNLLGLQRSSNFQCKLLWQLNGRLCYCLKDRMNFDPPEIKQLQNFsKEDAALTY 60
Db 1 msynllglqrssnfqckllwqlngrlcyckdrnmfdppeeikqlqfqkedaaltiy 60
Qy 61 EMLQNIFAIRQDSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
Db 61 emlqnifafrqdsstgwnetivenllanyvqhnhlktvleeklekedftrgklmssl 120
Qy 121 HLKRYGRIILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
Db 121 hlkrvgriilhyllkakeyshcawtivrveilrnfynrltgyln 166

RESULT 4
AAP50279
ID AAP50279 standard; protein; 166 AA.
XX
AC AAP50279;
XX
DT 09-DEC-1991 (first entry)
XX
DE Protein sequence encoding synthetic interferon-beta gene.
XX
KW Interferon-beta; virucide; antitumor; immunostimulant.
XX
OS Synthetic.
XX
PN EP131816-A.
XX
PD 23-JAN-1985.
XX
XX 28-JUN-1984; 84EP-0107498.
XX
XX 01-JUL-1983; 83GB-0017880.
XX
```

```
XX PA (SEAR ) SEARLE G D & CO.
XX PI Bell LD, Boseley PG, Smith JC, Houghton M;
XX XX
XX DR WPI; 1985-020165/04.
XX DR N-PSDB; AAN50306.
XX XX
XX PT New modified beta-interferon(s) - useful as antiviral,
XX PT anti-neoplastic and immuno-modulatory agents.
XX XX
XX PS Disclosure; Fig 20; 96pp; English.
XX PS
XX CC The sequence encodes a synthetic interferon-beta which has
XX CC increased biological activity compared to natural IFN-beta, and
XX CC which is more effective in the treatment of viral or neoplastic
XX CC diseases, or immunosuppressed or immunodeficient conditions.
XX XX
XX SQ Sequence 166 AA;

Query Match 98.9%; Score 864; DB 6; Length 166;
Best Local Similarity 98.8%; Pred. No. 1.5e-67;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSYNLLGLQRSSNFQCKLLWQLNGRLCYCLKDRMNFDPPEIKQLQNFsKEDAALTY 60
Db 1 msynllglqrssnfqckllwqlngrlcyckdrnmfdppeeikqlqfqkedaaltiy 60
Qy 61 EMLQNIFAIRQDSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
Db 61 emlqnifafrqdsstgwnetivenllanyvqhnhlktvleeklekedftrgklmssl 120
Qy 121 HLKRYGRIILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
Db 121 hlkrvgriilhyllkakeyshcawtivrveilrnfynrltgyln 166

RESULT 5
AAP61071
ID AAP61071 standard; Protein; 166 AA.
XX
AC AAP61071;
XX
DT 28-MAY-1991 (first entry)
XX
DE Oxidation resistant mutein of Interferon-Beta.
XX
KW IL-2; IFN-Beta; colony stimulating factor; CSF-1; tPA; hGF.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 1..6
XX FT /note= "May be N-terminal truncated or absent"
XX FT Misc-difference 17
XX FT /note= "May be any conservative AA"
XX FT Misc-difference 36
XX FT /note= "May be any conservative AA"
XX FT Misc-difference 62
XX FT /note= "May be any conservative AA"
XX FT Misc-difference 117
XX FT /note= "May be any conservative AA"
XX
XX AU8652451-A.
XX
XX 31-JUL-1986.
XX
XX 17-JAN-1986; 86AU-0052451.
XX
XX 17-DEC-1985; 85US-0810656.
XX PR 18-JAN-1985; 85US-0692596.
XX PR 05-NOV-1986; 86AU-0064846.
XX PR 05-AUG-1986; 86US-0893186.
XX
```

PA (CETU) CETUS CORP.
 XX Koths KE, Halenbeck RF, Innis MA;
 PI
 XX WPI; 1986-239075/37.
 DR
 XX Oxidn. resistant muten(s) - prepd. by replacing
 PT oxidn.-susceptible methionine with conservative aminoacid
 XX
 PS Claim 5; Page 50; 50pp; English.
 XX
 CC Modified peptide has residues susceptible to chloramine T and
 CC peroxide oxidation replaced with conservative AAs. Mutein is thus
 CC resistant to oxidation. Other proteins which may be similarly
 CC rendered resistant include tissue plasminogen activator, colony
 CC stimulating factor and human growth factor.
 XX
 SQ Sequence 166 AA;

Query Match 98.9%; Score 864; DB 7; Length 166;
 Best Local Similarity 98.8%; Pred. No. 1.5e-67;
 Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGLQRSSNFQCKLLWQLNGRLCYCLKDRMNFEDIPEIKQLQNFskEDAALTYI 60
 Db 1 msynllglqrssnfqckllwqlngrlcyleyckldrmnfedipeekqlqgfkedaaltiy 60
 QY 61 EMLQNIFAIRQDSSSTGWNETIVENLIANYVHQINHLKTVLEEKLEKEDFTRGKLMSL 120
 Db 61 emlqnifafrqdsstgwnetivenlianyvqhnhlktvleeklekedftrgklmsl 120
 QY 121 HLKRYGRILHYLKAKESYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
 Db 121 hlkrvgrilhyllkakeyshcawtivrveilrnfynrltgyln 166

RESULT 6
 AAP70296
 ID AAP70296 standard; protein; 166 AA.
 XX
 AC AAP70296;
 XX
 DT 07-JUN-1991 (first entry)
 XX
 DE Sequence of interferon-beta.
 KW Antiviral; antiproliferative agent.
 XX
 OS Homo sapiens.
 XX
 PN EP237019-A.
 XX
 PD 16-SEP-1987.
 XX
 PF 10-MAR-1987; 87EP-0103406.
 XX
 PR 14-MAR-1986; 86JP-0054650.
 PR 26-DEC-1986; 86JP-0308693.
 XX
 PA (TORA) TORAY IND INC.
 XX
 PI Tanaka T, Kawano G, Sawada R;
 XX
 DR WPI; 1987-258309/37.
 XX
 CC Conjugates of interferon(s)-beta and-gamma - useful as antivirals
 PT and anti-cell proliferatives with broader spectrum of activity
 PT and obtd. economically by recombinant DNA procedures
 XX
 PS Claim 7; p35; 52pp; English.
 XX
 CC The inventors claim an interferon conjugate wherein a C-terminal of

CC the region exhibiting biological activities of interferon-beta has
 CC been linked to an N-terminal of the region exhibiting biological
 CC activities of interferon-gamma. The antiviral activity of the
 CC conjugate was tested using FL cells-sindbis virus system according
 CC to the CPE 50 inhibition method. Antiviral activity ranged from
 CC 200 U/ml to 18500 U/ml.
 XX
 SQ Sequence 166 AA;

Query Match 98.9%; Score 864; DB 8; Length 166;
 Best Local Similarity 98.8%; Pred. No. 1.5e-67;
 Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGLQRSSNFQCKLLWQLNGRLCYCLKDRMNFEDIPEIKQLQNFskEDAALTYI 60
 Db 1 msynllglqrssnfqckllwqlngrlcyleyckldrmnfedipeekqlqgfkedaaltiy 60
 QY 61 EMLQNIFAIRQDSSSTGWNETIVENLIANYVHQINHLKTVLEEKLEKEDFTRGKLMSL 120
 Db 61 emlqnifafrqdsstgwnetivenlianyvqhnhlktvleeklekedftrgklmsl 120
 QY 121 HLKRYGRILHYLKAKESYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
 Db 121 hlkrvgrilhyllkakeyshcawtivrveilrnfynrltgyln 166

RESULT 7
 AAW81774
 ID AAW81774 standard; protein; 166 AA.
 XX
 AC AAW81774;
 XX
 DT 29-JAN-1999 (first entry)
 XX
 DE Human native interferon-beta protein.
 XX
 KW Interferon-Beta; variant; human; medicament; treatment; screening;
 KW multiple sclerosis; measurement; water soluble.
 XX
 OS Homo sapiens.
 XX
 PN DE19717864-A1.
 XX
 PD 29-OCT-1998.
 XX
 PF 23-APR-1997; 97DE-1017864.
 XX
 PR 23-APR-1997; 97DE-1017864.
 XX
 PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
 XX
 PI Otto B, Schneider-Presenius C, Waschuetza G;
 XX
 DR WPI; 1998-569784/49.
 XX
 PT New mutated recombinant human interferon-beta protein contains
 PT hydroxylic amino acid substitutions to improve water solubility -
 PT used e.g. in in vitro screening assays, to measure interferon levels
 PT and to treat multiple sclerosis
 XX
 PS Disclosure; Fig 1; 18pp; German.
 XX
 CC This sequence represents a native human recombinant interferon-beta
 CC protein which is mutated into an amino acid having at least one hydroxy
 CC group substituted for at least one of Leu5, Phe8, Phe15, Leu47, Phe50,
 CC Leu106, Phe111, Leu116, Leu120 and Phe156. Such mutants can be used in
 CC medicaments e.g. for treating multiple sclerosis, for in vitro screening
 CC assays and for measurement of interferon levels. The mutated protein is
 CC more water-soluble than recombinant wild-type human interferon-beta.
 XX
 SQ Sequence 166 AA;

| | | | | |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match | 98.9% | Score 864; | DB 19; | Length 166; |
| Best Local Similarity | 98.8% | Pred. No. 1.5e-67; | | |
| Matches 164; | Conservative 0; | Mismatches 2; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|---|-----|
| Qy | 1 | MSYNLLGFLGRSSNFQCKLQWLQNGRLREYCLCKORMNFDIPETIKQLQNFKEDAAALTY | 60 |
| | | | |
| | | | |
| | | | |
| | | | |
| Db | 1 | msynllgflgrssnfqckllwqlngrlreyclckdrnmfdipeelkqlqgfkedaaaltiy | 60 |
| | | | |
| | | | |
| | | | |
| | | | |
| Qy | 61 | EMLQNTAIPRODSSSTGWNETIVENLLANNVYHQINHLKTVLEKLEKEDTTRGKLMSSL | 120 |
| | | | |
| | | | |
| | | | |
| | | | |
| Db | 61 | emlqnifairfqdssstgwnetivenllannvyhginhlkvtleeklekedftrgklmssl | 120 |
| | | | |
| | | | |
| | | | |
| | | | |
| Qy | 121 | HLKRYGRIILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN | 166 |
| | | | |
| | | | |
| | | | |
| | | | |
| Db | 121 | hlkryvgriilhykakeyshcawtivrveilrnfynrltgylrn | 166 |
| | | | |
| | | | |
| | | | |
| | | | |

| | |
|----------|--|
| RESULT | 8 |
| AAE10346 | |
| ID | AAE10346 standard; Protein; 166 AA. |
| XX | |
| AC | AAE10346; |
| XX | |
| DT | 10-DEC-2001 (first entry) |
| XX | |
| XX | Mature human beta-interferon. |
| XX | |
| KW | Human; beta-interferon; INF-beta; immune disease; demyelinating disease; |
| KW | sub-acute sclerosing panencephalomyelitis; SSPE; multiple sclerosis; |
| KW | metachromatic leukodystrophy; Guillain-Barre syndrome; |
| KW | autoimmune disease. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| Key | Location/Qualifiers |
| FT | Misc-difference 162 |
| FT | /note= "Encoded by CGT" |
| XX | |
| PN | EP1133997-A2. |
| XX | |
| PD | 19-SEP-2001. |
| XX | |
| XX | 20-FEB-2001; 2001EP-0103580. |
| XX | |
| PR | 23-FEB-2000; 2000EP-0440053. |
| PR | 07-NOV-2000; 2000US-0246089. |
| XX | |
| PA | (TRGE) TRANSGENE SA. |
| XX | |
| PI | Braun S; |
| XX | |
| DR | WPI; 2001-572706/65. |
| DR | N-PSDB; AAD17506. |
| XX | |
| PT | Use of nucleic acid for the treatment of immune diseases such as |
| PT | multiple sclerosis - |
| XX | |
| PS | Claim 9; Page 15; 21pp; English. |
| XX | |
| CC | The invention relates to use of nucleic acids expressing human |
| CC | beta-interferon (INF-beta) for the treatment of immune diseases such as |
| CC | demyelinating disease (e.g. sub-acute sclerosing panencephalomyelitis |
| CC | (SSPE), metachromatic leukodystrophy, Guillain-Barre syndrome) and |
| CC | autoimmune disease (e.g. multiple sclerosis). The expression of the |
| CC | beta-interferon results in the improvement of the clinical status of |
| CC | the treated mammal, thus avoiding the use of recombinant polypeptide. |
| CC | The nucleic acid is therefore compatible with the quality of life of the |
| CC | patients. The present sequence is mature human beta-interferon. |
| XX | |
| SQ | Sequence 166 AA; |

| | | | | |
|-----------------------|--|--|-----------|-------------|
| Query Match | 98.98; | Score 864; | DB 22; | Length 166; |
| Best Local Similarity | 98.8%; | Pred. No. 1.5e-67; | | |
| Matches 164; | Conservative 0; | Mismatches 2; | Indels 0; | Gaps |
| | | | | |
| Qy | 1 | MSYNLLGFLQRSSNFQCCQLLWQLNGRLLEYCLKDRMNFDPPEETKQLQNFSKEDAALTIY 60 | | |
| Db | 1 | msynllgflqrssnfqccqlwqlnglrleyclkdrrnfdipeeikqlqgfkedaalitiy 60 | | |
| | | | | |
| Qy | 61 | EMLNQIFAIRQDSSSTGWNETIVENLLANYHQNHLKTVLEEKLEKEDFTRGKLMSL 120 | | |
| Db | 61 | emlnqifaifqdsstgwnetivenllanyvqhnhlktvleeklekedftrgklmsl 120 | | |
| | | | | |
| Qy | 121 | HLKRYGRIILHYLKAKEYSHCAWTVRVEILRNFFYNRLTGYLRN 166 | | |
| Db | 121 | hlkryygrilhyllkakeyshcawtivrveilrnfynrltgyln 166 | | |
| | | | | |
| RESULT | 9 | | | |
| AAE11979 | | | | |
| ID | AAE11979 | standard; Protein; 166 AA. | | |
| XX | XX | | | |
| AC | AAE11979; | | | |
| XX | XX | | | |
| DT | 18-DEC-2001 | (first entry) | | |
| XX | XX | | | |
| DE | Human | wild-type interferon (IFN) beta. | | |
| XX | XX | | | |
| KW | Human; interferon-gamma; IFNG; interferon-beta; Interferon alpha; FSH; | | | |
| KW | follicle stimulating hormone; granulocyte colony stimulating factor; | | | |
| KW | G-CSF; interleukin 10; IL-10; medicament; pulmonary administration; | | | |
| KW | circulatory administration. | | | |
| XX | XX | | | |
| OS | Homo sapiens. | | | |
| XX | XX | | | |
| PN | WO200168141-A2. | | | |
| XX | XX | | | |
| PD | 20-SEP-2001. | | | |
| XX | XX | | | |
| PF | 16-MAR-2001; 2001WO-DK00182. | | | |
| XX | XX | | | |
| PR | 17-MAR-2000; 2000DK-0000447. | | | |
| PR | 20-MAR-2000; 2000US-190844P. | | | |
| PR | 25-AUG-2000; 2000WO-DK00471. | | | |
| PR | 13-NOV-2000; 2000WO-DK00631. | | | |
| XX | XX | | | |
| PA | (MAXY-) MAXYGEN APS. | | | |
| XX | XX | | | |
| PI | Hansen CK; | | | |
| XX | XX | | | |
| DR | WPI; 2001-616274/71. | | | |
| XX | XX | | | |
| PT | Dispersions of particles for administration to the lung and circulatory | | | |
| PT | system by inhalation, e.g. from a nebulizer - | | | |
| XX | XX | | | |
| PS | Claim 22; Page 136; 139pp; English. | | | |
| XX | XX | | | |
| CC | The present invention relates to novel dispersions of a conjugate | | | |
| CC | comprising at least one non-polypeptide moiety covalently attached | | | |
| CC | to a polypeptide variant, wherein the amino acid sequence of the | | | |
| CC | polypeptide variant differs from that of the corresponding wild-type | | | |
| CC | human polypeptide in that at least 1 residue comprising an attachment | | | |
| CC | group for the non-polypeptide group has been introduced and/or removed. | | | |
| CC | The wild-type human polypeptide is selected from the group consisting | | | |
| CC | of interferon-gamma (IFNG), interferon-beta, interferon alpha, follicle | | | |
| CC | stimulating hormone, (FSH), interleukin 10 (L-10) and granulocyte colony | | | |
| CC | stimulating factor (G-CSF). The dispersion is used for the preparation | | | |
| CC | of a medicament for pulmonary and/or circulatory administration. The | | | |
| CC | present sequence is human wild type interferon (IFN) beta. | | | |
| XX | XX | | | |
| SQ | Sequence | 166 AA; | | |

| Query Match | Score 864 | DB 22 | Length 166 |
|-------------|-----------|-------|------------|
| 98.98 | | | |

PS Claim 11; Page - ; 108pp; English.

XX The sequence represents Human interferon beta mutant Q49K.

CC Conjugates of the invention exhibiting interferon beta activity

CC comprise at least one first non-polypeptide group covalently attached

CC to an interferon beta polypeptide, the amino acid sequence of which

CC differs from wild-type human interferon beta in at least one introduced

CC and at least one removed amino acid residue comprising an attachment

CC group for the first non-polypeptide group. The invention also concerns

CC reducing the immunogenicity and/or increasing functional in vivo

CC half-life and/or serum half-life of an interferon beta polypeptide

CC comprising introducing an amino acid residue constituting an attachment

CC group for a first non-polypeptide group into a position exposed at the

CC surface of the protein that does not contain such a group and removing

CC an amino acid residue constituting an attachment group for a first

CC non-polypeptide group and subjecting the modified peptide to conjugation

CC with the non-polypeptide group. The conjugate and a cell culture

CC expressing the mutated polypeptides are useful in the treatment of

CC disease, especially multiple sclerosis, and for treating mammals having

CC circulating antibodies against interferon beta la or lb. DNA encoding the

CC mutated proteins may be used for gene therapy. The DNA and proteins can

CC also be used to treat viral infections (e.g. viral hepatitis), cancer

CC (e.g. breast cancer), inflammation, Crohn's disease, acute myeloid

CC leukaemia, Hodgkin's disease and ulcerative colitis and for

CC immunomodulation.

CC Note: The present sequence is not shown in the specification but is

CC derived from the human interferon beta sequence given in AAU00038.

XX

SQ Sequence 166 AA;

Query Match 98.9%; Score 864; DB 22; Length 166;

Best Local Similarity 98.8%; Pred. No. 1.5e-67;

Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLGLFQRSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEIKQLQNFskEDAALTIY 60

Db 1 msynllglfqrssnfqckllwqlngrleyclckdrmmfdipeekqlqfkqedaaltiy 60

QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120

Db 61 emlqnifaifqdsstgwnetivenllanvyhqinhkltvleeklekedftrgklmssl 120

QY 121 HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFYINRLTGYLRN 166

Db 121 hlkrvygrilhyllkakeyshcawtivrveilrnfyinrltgyln 166

RESULT 12

AAB49356

ID AAB49356 standard; Protein; 166 AA.

XX AAB49356;

AC AAB49356;

XX

DT 07-MAR-2001 (first entry)

XX Human INF-beta A-chain.

DE Interferon-beta activity; multiple sclerosis; cancer; viral infection;

DE analogue.

KW Homo sapiens.

OS

XX WO200068387-A2.

PN

XX 16-NOV-2000.

PD

XX 12-MAY-2000; 2000WO-US13216.

PF

XX 12-MAY-1999; 99US-0133785.

PR

XX (XENC-) XENCOR INC.

PA

XX Bentzien J;

XX WPI; 2001-007398/01.

XX Novel interferon-beta activity (IbA) proteins which have greater

PT stability than interferon-beta (IFN-beta) useful for the treatment of

PT IFN-beta related disorders such as multiple sclerosis -

PI Bentzien J;

XX WPI; 2001-007398/01.

DR

XX Novel interferon-beta activity (IbA) proteins which have greater

PT stability than interferon-beta (IFN-beta) useful for the treatment of

PT IFN-beta related disorders such as multiple sclerosis -

XX

PS Disclosure; Fig 1A; 109pp; English.

XX The present invention provides proteins which have interferon-beta

CC (IFN-beta) activity. These analogues are produced so that they are less

CC than 97% identical to human IFN-beta. They are useful in the treatment of

CC multiple sclerosis, cancer, particularly osteosarcoma, basal cell

CC carcinoma, cervical dysplasia, glioma, acute myeloid leukaemia, multiple

CC myeloma, Hodgkin's disease, melanoma, and renal, liver and breast

CC cancers, viral infections, including those caused by hepatitis viruses,

CC herpes viruses and papilloma viruses, viral encephalitis, cytomegalovirus

CC pneumonia and prophylaxis of rhinovirus, idiopathic pulmonary fibrosis

CC and inflammatory diseases.

XX

SQ Sequence 166 AA;

Query Match 98.9%; Score 864; DB 22; Length 166;

Best Local Similarity 98.8%; Pred. No. 1.5e-67;

Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLGLFQRSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEIKQLQNFskEDAALTIY 60

Db 1 msynllglfqrssnfqckllwqlngrleyclckdrmmfdipeekqlqfkqedaaltiy 60

QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120

Db 61 emlqnifaifqdsstgwnetivenllanvyhqinhkltvleeklekedftrgklmssl 120

QY 121 HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFYINRLTGYLRN 166

Db 121 hlkrvygrilhyllkakeyshcawtivrveilrnfyinrltgyln 166

RESULT 13

AAB49357

ID AAB49357 standard; Protein; 166 AA.

XX AAB49357;

AC AAB49357;

XX

DT 07-MAR-2001 (first entry)

XX Human INF-beta B-chain.

DE Interferon-beta activity; multiple sclerosis; cancer; viral infection;

DE analogue.

KW Homo sapiens.

OS

XX WO200068387-A2.

PN

XX 16-NOV-2000.

PD

XX 12-MAY-2000; 2000WO-US13216.

PF

XX 12-MAY-1999; 99US-0133785.

PR

XX (XENC-) XENCOR INC.

PA

XX Bentzien J;

XX WPI; 2001-007398/01.

XX Novel interferon-beta activity (IbA) proteins which have greater

PT stability than interferon-beta (IFN-beta) useful for the treatment of

PT IFN-beta related disorders such as multiple sclerosis -

XX Example 1; Fig 1B; 109pp; English.

XX The present invention provides proteins which have interferon-beta

XX (IFN-beta) activity. These analogues are produced so that they are less

CC than 97% identical to human IFN-beta. They are useful in the treatment of

CC multiple sclerosis, cancer, particularly osteosarcoma, basal cell

CC carcinoma, cervical dysplasia, glioma, acute myeloid leukaemia, multiple

CC myeloma, Hodgkin's disease, melanoma, and renal, liver and breast

CC cancers, viral infections, including those caused by hepatitis viruses,

CC herpes viruses and papilloma viruses, viral encephalitis, cytomegalovirus

CC pneumonia and prophylaxis of rhinovirus, idiopathic pulmonary fibrosis

CC and inflammatory diseases.

XX Sequence 166 AA;

SQ

Query Match 98.9%; Score 864; DB 22; Length 166;

Best Local Similarity 98.8%; Pred. No. 1.5e-67;

Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGLQRSSNFQCKLLWQLNGRLCYCLKDRMNFDPPEIKQLQNFSKEDAALTIY 60

Db 1 msynllglqrssnfqckllwqlngrrleyclckdrnmfdipeeklqlqfqkedaaltiy 60

QY 61 EMLQNIFAIFRODSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSL 120

Db 61 emlqnifaifrqdssstgwnetivenllanyhqnihlktvleeklekedftrgklmsl 120

QY 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLRLN 166

Db 121 hlkrvgrrilhyllakeyshcawtivrveilrnffinrltgyrlrn 166

RESULT 14

AAP50261

ID AAP50261 standard; Protein; 177 AA.

XX AAP50261;

XX 20-NOV-1991 (first entry)

XX Sequence of beta-interferon (beta-IFN).

XX Expression vector; trp promoter-operator; transformed bacteria.

XX Homo sapiens.

XX US4499188-A.

XX 12-FEB-1985.

XX 05-MAY-1982; 82US-0375098.

XX 05-MAY-1982; 82US-0375098.

XX 23-JAN-1984; 84CA-0445883.

XX (CETU-) CETUS CORP.

XX (CETU) CETUS CORP.

XX Konrad MW, Mark DF;

XX WPI; 1985-055962/09.

XX N-PSDB; AAN50267.

XX Polypeptide, esp. interferon, prodn. by transformed bacteria -

PT cultured in presence of a repressor which is consumed during

PT growth

XX Example; Fig 2; 12pp; English.

XX The inventors claim a process for the prodn. of heterologous

CC polypeptide by transformed bacteria. The pref. promoter-operator is

CC trp which controls expression of structural genes encoding

CC polypeptides of a synthetic pathway forming tryptophan, esp. at a

CC concn. of 5.3r mg/l (T= predetermined turbidity value measured at

CC 680nm, esp. 10-100). The transformed bacteria are esp. E.coli contg.

CC the plasmid p-beta-1-trp. Example 1 concerns the construction of

CC plasmid p-beta-1-trp for the direct expression of IFN-beta under the

CC control of trp promoter-operator.

XX Sequence 177 AA;

SQ

Query Match 98.9%; Score 864; DB 6; Length 177;

Best Local Similarity 98.8%; Pred. No. 1.6e-67;

Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGLQRSSNFQCKLLWQLNGRLCYCLKDRMNFDPPEIKQLQNFSKEDAALTIY 60

Db 12 msynllglqrssnfqckllwqlngrrleyclckdrnmfdipeeklqlqfqkedaaltiy 71

QY 61 EMLQNIFAIFRODSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSL 120

Db 72 emlqnifaifrqdssstgwnetivenllanyhqnihlktvleeklekedftrgklmsl 131

QY 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLRLN 166

Db 132 hlkrvgrrilhyllakeyshcawtivrveilrnffinrltgyrlrn 177

RESULT 15

AAY84920

ID AAY84920 standard; Protein; 183 AA.

XX AAY84920;

XX 21-AUG-2000 (first entry)

XX Amino acid sequence of a His-tagged interferon beta la protein.

XX Interferon beta la; IFN-beta; polymer; polyalkylene glycol; tumour;

XX cancer; autoimmune condition; fibrosis; lupus; multiple sclerosis;

XX viral disease; anglogenic disease.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1..4

FT /label= 9

FT /note= "His tag"

FT Peptide 10..12

FT /note= "spacer"

FT Protein 18..183

FT /note= "natural interferon-beta"

XX WO200023114-A2.

XX 27-APR-2000.

XX 15-OCT-1999; 99WO-US24201.

XX 16-OCT-1998; 98US-0104572.

XX 16-FEB-1999; 99US-0120161.

XX (BIOJ) BIOGEN INC.

XX Pepinsky B, Runkel L, Brickelmaier M, Whitty A, Hochman P;

XX WPI; 2000-339534/29.

XX N-PSDB; AAA15062.

XX New glycosylated interferon-beta-la coupled to a non-naturally

PT occurring polymer containing a polyalkylene glycol useful for treating

PT e.g. tumors, autoimmune disorders, viral infections and angiogenic

```
PT diseases -
XX
PS Example 1: Fig 10: 73pp; English.
XX
CC The present sequence represents a His-tagged interferon beta la
CC (IFN-beta) protein. The protein is used to produce a composition
CC comprising a glycosylated IFN-beta coupled to a non-naturally-occurring
CC polymer containing a polyalkylene glycol. The composition has enhanced
CC activity, measured by an antiviral assay, as compared to physiologically
CC active IFN-beta. The polymer-IFN-beta conjugate has the ability to
CC stay in the vasculature for longer periods of time, has increased
CC stability in solution, reduced immunogenicity, protection of the modified
CC IFN-beta-la from proteolytic digestion and subsequent abolition activity,
CC and increased thermal stability. The polymer-based conjugates are useful
CC for treating tumors and cancer, as well as autoimmune conditions such
CC as fibrosis, lupus and multiple sclerosis. These may also be used in the
CC treatment of viral diseases, as well as in the treatment of angiogenic
CC diseases. IFN-beta is useful as an agent for the treatment, remission
CC or attenuation of a disease state, physiological condition, symptoms or
CC etiological factors, or for their evaluation or diagnosis. The IFN-beta
CC polymer conjugates may also be used for prophylaxis or treatment of any
CC condition or disease state for which the IFN-beta constituent is
CC efficacious, in biological systems or specimens.
XX
SQ Sequence 183 AA;

Query Match          98.9%; Score 864; DB 21; Length 183;
Best Local Similarity 98.8%; Pred. No. 1.6e-67;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLGLFQRSNFQCQKLLWQLNGRLEYCLKDRMNFDPETKQLQnFSKEDAALTYI 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 18 msynllglqrsnfcqckllwqlngrleyclckdrnmfdipeelkqgfkedaaltiy 77
   |||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 EMLQNIFAIFRQDSSSTGWNFTIVENLLANVYHQINHLKTVLEEKLEKEDFTRGLMSSL 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 78 emlqnfaifrqqssstgwnftivenllanvyhqinhktvleeklekedftrgklmssl 137
   |||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 HLKRYYGRILHYLKKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 138 hlkrvyygrilhylkakeyshcawtivrveillrnfyfinrltgylrn 183
   |||||||||||||||||||||||||||||||||||||||||||||||||||

Search completed: July 29, 2002, 15:42:54
Job time: 230 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2002, 15:41:34 ; Search time 46.62 Seconds
(without alignments)
615.984 Million cell updates/sec

Title: SEQ2-49N-51S
Perfect score: 874
Sequence: 1 MSNLLGLFQRSSNFQCKL.....RVEILRNFYFINRLTGYLRN 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_19.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 822 | 94.1 | 187 | 6 | 077812 macaca fasc |
| 2 | 817 | 93.5 | 187 | 4 | Q15943 homo sapien |
| 3 | 525.5 | 60.1 | 186 | 6 | Q29412 sus scrofa |
| 4 | 255.5 | 29.2 | 195 | 6 | Q9GLL5 bos taurus |
| 5 | 250.5 | 28.7 | 189 | 4 | Q14618 homo sapien |
| 6 | 245.5 | 28.1 | 188 | 4 | Q96K16 bos sapien |
| 7 | 245 | 28.0 | 195 | 6 | Q28844 oryctolagus |
| 8 | 244 | 27.9 | 189 | 6 | Q95J78 saguinus oe |
| 9 | 242 | 27.7 | 189 | 6 | Q95J77 saguinus oe |
| 10 | 241.5 | 27.6 | 189 | 4 | Q14607 homo sapien |
| 11 | 239.5 | 27.4 | 195 | 6 | Q9GLL6 homo sapien |
| 12 | 237 | 27.1 | 174 | 4 | Q13168 homo sapien |
| 13 | 237 | 27.1 | 195 | 6 | Q28845 oryctolagus |
| 14 | 237 | 27.1 | 195 | 6 | Q28562 ovis aries |
| 15 | 237 | 27.1 | 195 | 6 | Q28545 ovis aries |
| 16 | 236.5 | 27.1 | 189 | 4 | Q14639 homo sapien |

| | | | | | |
|----|-------|------|-----|----|--------------------|
| 17 | 236.5 | 27.1 | 195 | 6 | Q9MYK6 bos taurus |
| 18 | 236.5 | 27.1 | 195 | 6 | Q95NE2 bos taurus |
| 19 | 235 | 26.9 | 195 | 6 | Q28843 oryctolagus |
| 20 | 235 | 26.9 | 195 | 6 | Q28847 oryctolagus |
| 21 | 235 | 26.9 | 195 | 6 | Q28561 ovis aries |
| 22 | 226 | 25.9 | 190 | 6 | Q29085 sus scrofa |
| 23 | 225.5 | 25.8 | 179 | 6 | Q29084 sus scrofa |
| 24 | 223.5 | 25.6 | 195 | 6 | P28170 ovis aries |
| 25 | 221.5 | 25.3 | 181 | 4 | Q14608 homo sapien |
| 26 | 220 | 25.2 | 190 | 6 | Q29098 sus scrofa |
| 27 | 219 | 25.1 | 190 | 11 | Q9ES91 marmota mon |
| 28 | 218 | 24.9 | 166 | 4 | Q9UMJ3 homo sapien |
| 29 | 218 | 24.9 | 189 | 4 | Q14605 homo sapien |
| 30 | 215.5 | 24.7 | 207 | 4 | Q9P0W0 homo sapien |
| 31 | 213 | 24.4 | 190 | 11 | Q61719 mus musculu |
| 32 | 209 | 23.9 | 190 | 11 | Q9N822 marmota mon |
| 33 | 201 | 23.0 | 190 | 11 | O64138 cricetinae |
| 34 | 198 | 22.7 | 84 | 6 | Q95L88 sus scrofa |
| 35 | 195.5 | 22.4 | 170 | 6 | Q29114 sus scrofa |
| 36 | 194 | 22.2 | 190 | 11 | Q61718 mus musculu |
| 37 | 194 | 22.2 | 190 | 11 | Q91WX3 sigmodon hi |
| 38 | 193.5 | 22.1 | 170 | 6 | Q29115 sus scrofa |
| 39 | 188 | 21.5 | 108 | 6 | Q9N1U6 equus cabal |
| 40 | 187 | 21.4 | 166 | 6 | P79228 odocolleus |
| 41 | 186 | 21.3 | 190 | 11 | Q61716 mus musculu |
| 42 | 181 | 20.7 | 136 | 11 | Q61717 mus musculu |
| 43 | 148.5 | 17.0 | 193 | 13 | Q9PW15 gallus gall |
| 44 | 146.5 | 16.8 | 182 | 11 | Q9R1T0 mus musculu |
| 45 | 132.5 | 15.2 | 193 | 13 | Q9PW16 gallus gall |

ALIGNMENTS

RESULT 1

| | | | |
|--------|---|------|---------|
| 077812 | PRELIMINARY; | PRT; | 187 AA. |
| ID | 077812 | | |
| AC | 077812; | | |
| DT | 01-NOV-1998 (Tremblrel. 08, Created) | | |
| DT | 01-NOV-1998 (Tremblrel. 08, Last sequence update) | | |
| DT | 01-DEC-2001 (Tremblrel. 19, Last annotation update) | | |
| DE | INTERFERON BETA. | | |
| GN | IFN-BETA. | | |
| OS | Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; | | |
| OC | Cercopitheidae; Macaca. | | |
| OX | NCBI_TaxID=9541; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | MEDLINE=99156140; PubMed=10048395; | | |
| RA | Matheux F., Le Grand R., Rousseau V., De Maeyer E., Dormont D., | | |
| RA | Lauret E.; | | |
| RT | "Macaca lymphocytes transduced by a constitutively expressed | | |
| RT | interferon beta gene display an enhanced resistance to SIIVmac251 | | |
| RT | infection." | | |
| RT | infection." RT | | |
| RL | Hum. Gene Ther. 10:429-429(1999). | | |
| CC | -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA | | |
| CC | FAMILY. | | |
| DR | EMBL; AJ011909; CAA09862.1; -. | | |
| DR | HSSP; P01574; 1AU1. | | |
| DR | InterPro; IPR000471; Interferon_abd. | | |
| DR | Pfam; PF00143; Interferon; 1. | | |
| DR | PRINTS; PR00266; INTERFERONAB. | | |
| DR | ProDom; PD000550; Interferon_abd; 1. | | |
| DR | SMART; SM00076; IFabd; 1. | | |
| DR | PROSITE; PS00252; INTERFERON_A_B_D; 1. | | |
| KW | Antiviral; Cytokine. | | |
| SQ | SEQUENCE 187 AA; 22266 MW; 376AEF73332B7807 CRC64; | | |

Query Match 94.1%; Score 822; DB 6; Length 187;
Best Local Similarity 92.8%; Pred. No. 2e-63;


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Matches 154; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQSSNFQCKLLWQNGRLEYCLKDRMNFDPPEIKQLQNFsKEDAALTYI 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 22 MSYNLLGFLQSSNFQCKLLWQNGRLEYCLKDRMNFDPPEIKQLQNFsKEDAALTYI 81
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 EMLQNIFAIFQDSSSTGWNTEIVENLLANVYHQINHLKTVLEEKLEKEDFTGRKLMSSL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 82 EMLQNIYAIFQDLSSTGWNTEIVENLLANVYHQIDHLKTVLEEKLEKEDFTGRKFMSSL 141
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 HLKRYGGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTYGLRN 166
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 142 HLKRYGGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTYGLRN 187
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 2
Q15943 PRELIMINARY; PRT; 187 AA.
AC Q15943;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE INTERFERON-BETA PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065590; PubMed=6183692;
RA Fiers W., Remaut E., Devos R., Cheroutre H., Contreras R.R.,
RA Gheysen D., Degraeve W.M., Staussens P., Tavernier J., Taya Y.,
RA Content J.;
RT "The human fibroblast and human immune interferon genes and their
RT expression in homologous and heterologous cells.";
RL Philos. Trans. R. Soc. Lond. B, Biol. Sci. 295:29-38(1982).
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
DR EMBL; M23460; AAC41702.1; -.
DR HSSP; P01574; IAU1.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; UNKNOWN_1.
KW Antiviral; Cytokine; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 187 INTERFERON-BETA.
SQ SEQUENCE 187 AA; 22251 MW; D8EE65B94862061 CRC64;

Query Match 93.5%; Score 817; DB 4; Length 187;
Best Local Similarity 94.6%; Pred. No. 5,3e-63;
Matches 157; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQSSNFQCKLLWQNGRLEYCLKDRMNFDPPEIKQLQNFsKEDAALTYI 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 22 MSYNLLGFLQSSNFQCKLLWQNGRLEYCLKDRMNFDPPEIKQLQNFsKEDAALTYI 81
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 EMLQNIFAIFQDSSSTGWNTEIVENLLANVYHQINHLKTVLEEKLEKEDFTGRKLMSSL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 82 EMLQNIYAIFQDSSSTGWNTEIVENLLANVYHQINHLKTVLEEKLEKEDFTGRKRMSSL 141
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 HLKRYGGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTYGLRN 166
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 142 HLKRYGGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTYGLRN 187
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
Q29412 PRELIMINARY; PRT; 186 AA.
ID Q29412
AC Q29412;

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DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE INTERFERON-BETA-1 PRECURSOR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Artursson K., Gobl A., Lindersson M., Johansson M., Alm G.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92348930; PubMed=1640116;
RA Artursson K., Gobl A., Lindersson M., Johansson M., Alm G.;
RT "Molecular cloning of a gene encoding porcine interferon-beta.";
RL J. Interferon Res. 12:153-160(1992).
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
DR EMBL; M86762; AAA31056.1; -.
DR EMBL; S41178; AAB22723.1; -.
DR HSSP; P01574; IAU1.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
KW Antiviral; Cytokine; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 186 INTERFERON-BETA-1.
SQ SEQUENCE 186 AA; 21878 MW; 5F16B8B3C3AE603D CRC64;

Query Match 60.1%; Score 525.5; DB 6; Length 186;
Best Local Similarity 60.8%; Pred. No. 7.1e-38;
Matches 101; Conservative 28; Mismatches 36; Indels 1; Gaps 1;

QY 1 MSYNLLGFLQSSNFQCKLLWQNGRLEYCLKDRMNFDPPEIKQLQNFsKEDAALTYI 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 22 MSYDVLRYQQRSSNLACQLLGGTQCYCLEDRNFVEPPEIMQPPQKEDAVLIH 81
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 EMLQNIFAIFQDSSSTGWNTEIVENLLANVYHQINHLKTVLEEKLEKEDFTGRKLMSSL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 82 EMLQIIFGILRRNFSSGTGWNTEIVKTLVLDQGMDDLEILEEIMEENFPRGD-MTIL 140
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 HLKRYGGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTYGLRN 166
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 141 HLKRYLSILQYDKKEYRSCAWTVVQVVEILRNFFYNRLTYGLRN 186
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
Q9GLL5 PRELIMINARY; PRT; 195 AA.
AC Q9GLL5;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE INTERFERON TAU.
GN IFN-TAU-C1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Chung Y.G., Seidel G.E. Jr.;
RT "Cloning bovine interferon-tau genes and characterizing their
RT transcriptional expression during early pregnancy.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.

```


| | | | |
|---|--|--|--|
| DR | HSP: | P01563; | 2HIE. |
| DR | InterPro: | IPR000471; | Interferon_abd. |
| DR | Fam: | PF00143; | interferon; 1. |
| DR | PRINTS: | PD00266; | INTERFERONAB. |
| DR | ProDom: | PD000550; | Interferon_abd; 1. |
| DR | SMART: | SM00076; | Ifabd; 1. |
| DR | PROSITE: | PS00252; | INTERFERON_A_B_D; 1. |
| KW | Activitalr: | Cytokine. | |
| SQ | SEQUENCE | 195 AA; | 21981 MW; D4D2E3EF513AE5F CRC64; |
| | | | |
| Query Match 28.0%; Score 245; DB 6; Length 195; Best Local Similarity 41.1%; Pred. No. 1.le-13; Matches 51; Conservative 20; Mismatches 53; Indels 0; Gaps 0; | | | |
| QY | 31 | CLKDMRNFDIPEETKQLNFSKDAAALTIYEMLNIFAIERQDSSTGNETIVENLLAN | 90 : : : : : : : |
| Db | 52 | CLDKRRDPFFREVVNGSQKHVSVLHEMLQQIFNLHTAIISSAWNLTLEELHAA | 111 : : |
| QY | 91 | VYHOINHLTKVTLEEKEDETRFKLMSSLHKRLRYGRILHYLKAKKEYSHCAWTIVRVFI | 150 :: : : : : :: : : : : : |
| Db | 112 | LHQLOGLTCTLVAMGEEDSVLTADPTLMRKRYFORIRLYLDEKKHGCGAWELVRMEI | 171 : |
| QY | 151 | LRNF 154 | |
| Db | 172 | RRAF 175 | |
| <hr/> | | | |
| RESULT | 8 | | |
| Q95J78 | ID | PRELIMINARY; | PRT; 189 AA. |
| AC | Q95J78; | | |
| Dt | 01-DEC-2001 | (TrEMBLrel. 19, Created) | |
| Tl | DT | 01-DEC-2001 | (TrEMBRel. 19, Last sequence update) |
| Ox | 01-DEC-2001 | (TrEMBRel. 19, Last annotation update) | |
| De | INTERFERON-ALPHA PRECURSOR. | | |
| Gn | INF-ALPHA. | | |
| Os | Saguinus oedipus (Cotton-top tamarin). | | |
| Oc | Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi; | | |
| Ox | Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus. | | |
| Ox | NCB_I_TaxID=9490; | | |
| Rn | [1] | | |
| Rp | SEQUENCE FROM N.A. | | |
| Ra | Ceccacci A., Aurisicchio L., Ciliberto G., Palombo F., Traboni C.; | | |
| Rt | "Recombinant cotton-top tamarin interferon: a new tool for a primate hepatitis model." | | |
| Rl | Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. | | |
| Dr | EWB1; AJ250195; CAG4424.1; -. | | |
| Kw | Signal. | | |
| Ft | SIGNAL | 1 23 POTENTIAL. | |
| Ft | CHAIN | 24 189 POTENTIAL. | |
| Sq | SEQUENCE | 189 AA; 21937 MW; 06A45DD2B631C85C CRC64; | |
| | | | |
| Query Match 27.9%; Score 244; DB 6; Length 189; Best Local Similarity 33.3%; Pred. No. 1.3e-13; Matches 54; Conservative 29; Mismatches 65; Indels 14; Gaps 1; | | | |
| QY | 5 | LLGFQRSSNPQCOKLLWLGNRIEYLCKLDNRNDTFDIPEIKQLDNFKSKEDAALIYEMIQ | 64 : : : : : : : : : : : : : : |
| Db | 40 | LLAQMRSISFP-----CLKRDREFEQEEFGNQFOKARAFVLHEMIQ | 85 : : : : : : : : : : : : : : |
| QY | 65 | NIFAIRQDSSTGWNETIVENLLANYTHOINHUKTVLEEKLXEDFTRGKLMSSLHLKR | 124 : |
| Db | 86 | QTFLNLSKTOSSAWDDEFLLDFTELYQQUNELCACVVGVEGVTDPLLEDNSILLTVRK | 145 : |
| QY | 125 | YYGRILHYLKAKKEYSHCAWTIVRVFIERNFNFFINRLTGYLERN | 166 : |
| Db | 146 | YFQITLYLNEKKYSACAVEVRAEIHRSFSLTNLQGILRS | 187 : |
| RESULT | 9 | | |
| Q95J77 | ID | PRELIMINARY; | PRT; 189 AA. |

```
Query Match      27.6%; Score 241.5; DB 4; Length 189;
Best Local Similarity 37.4%; Pred. No. 2.2e-13;
Matches 58; Conservative 22; Mismatches 58; Indels 17; Gaps 4;

QY 20 LLWLQNLRL--YCLKDRMNFDPPEIKQLQNFskEDAALTYEMLQNFIFAIFRODSSST 77
DB 40 LLAQNM-GRISPFSCDKRHEFRPEEFDFGHQFQKTAISVLHEMIQOQTFNLFSTEDSSA 98
QY 78 GWNETIVENLLANYHQINHLKT-----VLEEKLEKEDFTRGKLMSSHLKRYGYRIL 130
DB 99 AWEQSLLEKSFELYQQLNDLACVYQEVGVETPLMNEFI-----LAVRKYQRIT 151
QY 131 HYLKAKKEYSHCAWTIVRVEILRNFYINRLTYLR 165
DB 152 LYLTEKYSKPCAWEVVRAEIMRSFSFSTNLKKGLR 186

RESULT 11
Q9GLL6 PRELIMINARY; PRT; 195 AA.
AC Q9GLL6;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE INTERFERON TAU.
GN IFN-TAU-C3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN SEQUENCE FROM N.A.
RA Chung Y.G., Seidel G.E. Jr.;
RT "Cloning bovine interferon-tau genes and characterizing their
transcriptional expression during early pregnancy.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
DB EMBL; AF238611; AAG14168.1; -.
DR HSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
KW Antiviral; Cytokine.
SQ SEQUENCE 195 AA; 22160 MW; 6DB1FAE39BF033FA CRC64;

Query Match      27.4%; Score 239.5; DB 6; Length 195;
Best Local Similarity 37.5%; Pred. No. 3.3e-13;
Matches 51; Conservative 29; Mismatches 53; Indels 3; Gaps 2;

QY 19 KLLWLQNLRL--EYCLKDRMNFDPPEIKQLQNFskEDAALTYEMLQNFIFAIFRODSSS 76
DB 39 RLLARMN-RLSPHPCQDRKDFGLPQEWVGGSQLQKDAISVLHEMLQOCFNLFHIEHSS 97
QY 77 TQWNETIVENLLANYHQINHLKTIVLEEKLEKEDFTRGKLMSSHLKRYGYRILHYLKAK 136
DB 98 AAWNTTLLQLCTGLQQLQEDLQACGLPVNGEKSDMGMRGPILTVMKYPFDIHVYLKEK 157
QY 137 EYSHCAWTIVRVEILR 152
DB 158 EYSDCAWEIIRVEMMR 173

RESULT 12
Q13168 PRELIMINARY; PRT; 174 AA.
ID Q13168
AC Q13168;
```

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DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE INTERFERON OMEGA-1 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RA Zeng Q., Li M., Zhou Y., Guo H., Hou Y.;
RT "The cloning, sequencing of the primary structure and expression in E.
coli Chinese human IFN-W1 gene.";
RL Sci. China B. 0:0-0(0).
RN [2]
RN SEQUENCE FROM N.A.
RA Xu L.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
DR EMBL; U25670; AAA70091.1; -.
DR HSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
FT NON_TER 1
SQ SEQUENCE 174 AA; 20249 MW; B1CC9AB5993016C5 CRC64;

Query Match      27.1%; Score 237; DB 4; Length 174;
Best Local Similarity 33.8%; Pred. No. 4.8e-13;
Matches 46; Conservative 32; Mismatches 58; Indels 0; Gaps 0;

QY 31 CLKDRMNFDPPEIKQLQNFskEDAALTYEMLQNFIFAIFRODSSSTGWNETIVENLLAN 90
DB 31 CLKDRRDFRPQEMVKGSQLKAHVMSALHEMLQOIFSLFHTERSAAWNMTLLQLHTG 90
QY 91 VYHQINHLKTIVLEEKLEKEDFTRGKLMSSHLKRYGYRILHYLKAKKEYSHCAWTIVRVEI 150
DB 91 LHQQLHLETCLLQVVGESAGAISSPALTLRRYFGIRVYLKBKYSDCAWEDRMEI 150
QY 151 LRNFYFINRLTYLRN 166
DB 151 MKSLFLSTNMOERLS 166

RESULT 13
Q28845 PRELIMINARY; PRT; 195 AA.
AC Q28845
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE INTERFERON-OMEGA45
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RN SEQUENCE FROM N.A.
RA MEDLINE=94132653; PubMed=8301151;
RA Charlier M., L'Hardon R., Boissard M., Martal J., Gaye P.;
RT "Cloning and structural analysis of four genes encoding interferon-
omega in rabbit.";
RL J. Interferon Res. 13:313-322(1993).
CC -|- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
DR EMBL; S69000; AAC60526.1; -.
DR HSP; P01563; 2HIE.
```

| | |
|--|--|
| DR | InterPro: IPR000471; Interferon_abd. |
| DR | Pfam: PF00143; Interferon; 1. |
| DR | PRINTS; PR00266; INTERFERONAB. |
| DR | ProDom; PD000550; Interferon_abd; 1. |
| DR | SMART; SM00076; IFabd; 1. |
| DR | PROSITE; PS00252; INTERFERON_A_B_D; 1. |
| KW | Antiviral; Cytokine; 1996 MW; 395EE700C586A928 CRC64; |
| SQ | SEQUENCE 195 AA; 21996 MW; 395EE700C586A928 CRC64; |
| Query Match 27.1%; Score 237; DB 6; Length 195; Best Local Similarity 39.5%; Pred. No. 5.5e-13; Matches 49; Conservative 20; Mismatches 55; Indels 0; Gaps 0; | |
| OY | 31 CLKDRMNFDPPEETKQLQNFskEDAALTIYEMLQNIFAIRFQDSSSTGNETIVENLLAN 90 : : : : : : : : : : : : : : : |
| DB | 52 CLKRRDFPFREVNGSQFNQTVSVLHMLQQIFNLLHTARSSAAWNNTLLEELHTA 111 : : : : : : : : : : : : : : : |
| OY | 91 VYHQINHLKTVLEKELEDTRGLKSSLHKRYGRILHYLKAKESHCATITVRVEI 150 :: : |
| DB | 112 LHOOLGLETCLVQAMGEEDSVLTADSPTLMLKRYFORIRLYLDEKKHGCAWLVRMEI 171 :: : |
| OY | 151 LRNP 154 |
| DB | 172 RRAF 175 |
| RESULT 14 Q28562 PRELIMINARY; PRT; 195 AA. ID AC Q28562 DT 01-NOV-1996 (Tremblrel. 01, Created) DT 01-NOV-1996 (Tremblrel. 01, Last sequence update) DT 01-DEC-2001 (Tremblrel. 19, Last annotation update) DE OVIN INTERFERON ALPHA PRECURSOR. OS Ovis aries (Sheep). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; OC Bovidae; Caprinae; Ovis. OX NCBI_TaxID=9940; RN [1] RP SEQUENCE FROM N.A. RX MEDLINE-96219886; PubMed-8639714; RA Liu L., Leaman D.W., Bixby J.A., Roberts R.M.; RT "A type I ovine interferon with limited similarity to IFN-alpha, IFN-omega and IFN-tau: gene structure, biological properties and unusual species specificity."; RL Biochim. Biophys. Acta, Gene Struct. Expr. 1294:55-62(1996). CC - - SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY CC EMBL; U26254; AAB06828.1; -. DR HSSP; P01563; ZHIE. DR InterPro; IPR000471; Interferon_abd. DR Pfam; PF00143; Interferon; 1. DR PRINTS; PR00266; INTERFERONAB. DR ProDom; PD000550; Interferon_abd; 1. DR SMART; SM00076; IFabd; 1. DR PROSITE; PS00252; INTERFERON_A_B_D; 1. KW Antiviral; Cytokine; Signal. FT SIGNAL 1 23 POTENTIAL. FT CHAIN 24 195 INTERFERON TYPE I. SQ SEQUENCE 195 AA; 22010 MW; 15C4CD45D582F8E6 CRC64; | |
| Query Match 27.1%; Score 237; DB 6; Length 195; Best Local Similarity 39.5%; Pred. No. 5.5e-13; Matches 49; Conservative 20; Mismatches 55; Indels 0; Gaps 0; | |
| OY | 31 CLKDRMNFDPPEETKQLQNFskEDAALTIYEMLQNIFAIRFQDSSSTGNETIVENLLAN 90 : : : : : : : : : : : : : : : |
| DB | 52 CLKRRDFPFREVNGSQFNQTVSVLHMLQQIFNLLHTARSSAAWNNTLLEELHTA 111 : : : : : : : : : : : : : : : |
| OY | 91 VYHQINHLKTVLEKELEDTRGLKSSLHKRYGRILHYLKAKESHCATITVRVEI 150 :: : |
| DB | 112 LHOOLGLETCLVQAMGEEDSVLTADSPTLMLKRYFORIRLYLDEKKHGCAWLVRMEI 171 :: : |
| OY | 151 LRNP 154 |
| DB | 172 RRAF 175 |
| RESULT 14 Q28562 PRELIMINARY; PRT; 195 AA. ID AC Q28562 DT 01-NOV-1996 (Tremblrel. 01, Created) DT 01-NOV-1996 (Tremblrel. 01, Last sequence update) DT 01-DEC-2001 (Tremblrel. 19, Last annotation update) DE OVIN INTERFERON ALPHA PRECURSOR. OS Ovis aries (Sheep). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; OC Bovidae; Caprinae; Ovis. OX NCBI_TaxID=9940; RN [1] RP SEQUENCE FROM N.A. RX TISSUE-LIVER. RC MEDLINE-92039090; PubMed-1937057; RA Whaley A.E., Carroll R.S., Inakawa K.; RT "Cloning and analysis of a gene encoding ovine interferon alpha-II."; RL Gene 106:281-282(1991). CC - - SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY CC EMBL; X59068; CAA41791.1; -. DR HSSP; P01563; ZHIE. DR InterPro; IPR000471; Interferon_abd. DR Pfam; PF00143; Interferon; 1. DR PRINTS; PR00266; INTERFERONAB. DR ProDom; PD000550; Interferon_abd; 1. DR SMART; SM00076; IFabd; 1. DR PROSITE; PS00252; INTERFERON_A_B_D; 1. KW Antiviral; Cytokine; Signal. FT SIGNAL 1 23 POTENTIAL. FT CHAIN 24 195 OVINE INTERFERON ALPHA. SQ SEQUENCE 195 AA; 22006 MW; 3B8EE700C586A928 CRC64; | |
| Query Match 27.1%; Score 237; DB 6; Length 195; Best Local Similarity 39.5%; Pred. No. 5.5e-13; Matches 49; Conservative 20; Mismatches 55; Indels 0; Gaps 0; | |

Search completed: July 29, 2002, 15:44:50
Job time: 196 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2002, 15:42:54 ; Search time 51.64 Seconds
(without alignments)
357.054 Million cell updates/sec

Title: SEQ2-49N-51T

Perfect score: 875

Sequence: 1 MSYNLLGFLQSSNFQCKL.....RVELRNFYFINRLTYGLRN 166

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_032802.*

- 1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
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- 7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|---------------------|
| 1 | 869 | 99.3 | 166 | 22 AAU00119 | Human interferon b |
| 2 | 866 | 99.0 | 166 | 22 AAU00103 | Human interferon b |
| 3 | 866 | 99.0 | 166 | 22 AAU00150 | Human interferon b |
| 4 | 863 | 98.6 | 166 | 4 AAP30219 | Sequence of interf |
| 5 | 863 | 98.6 | 166 | 6 AAP50262 | Sequence encoded b |
| 6 | 863 | 98.6 | 166 | 6 AAP50279 | Protein sequence e |
| 7 | 863 | 98.6 | 166 | 7 AAP61071 | Oxidation resistan |
| 8 | 863 | 98.6 | 166 | 8 AAP70296 | Sequence of interf |
| 9 | 863 | 98.6 | 166 | 19 AAH81774 | Human native interf |
| 10 | 863 | 98.6 | 166 | 22 AAEL0346 | Mature human beta- |
| 11 | 863 | 98.6 | 166 | 22 AAEL1979 | Human wild-type in |

| | | | | | |
|----|-----|------|-----|-------------|--------------------|
| 12 | 863 | 98.6 | 166 | 22 AAU00038 | Human interferon b |
| 13 | 863 | 98.6 | 166 | 22 AAU00074 | Human interferon b |
| 14 | 863 | 98.6 | 166 | 22 AAB49336 | Human INF-beta A-c |
| 15 | 863 | 98.6 | 166 | 22 AAB49337 | Human INF-beta B-c |
| 16 | 863 | 98.6 | 177 | 6 AAP50261 | Sequence of beta-1 |
| 17 | 863 | 98.6 | 183 | 21 AAY84920 | Amino acid sequenc |
| 18 | 863 | 98.6 | 183 | 21 AAY70866 | Histidine tagged-h |
| 19 | 863 | 98.6 | 187 | 2 AAP10016 | Sequence of fibrob |
| 20 | 863 | 98.6 | 187 | 3 AAP20026 | Human fibroblast 1 |
| 21 | 863 | 98.6 | 187 | 15 AAR56987 | Human interferon b |
| 22 | 863 | 98.6 | 187 | 19 AAW61154 | Human HCMV inducib |
| 23 | 863 | 98.6 | 187 | 20 AAY05380 | Human beta-interfe |
| 24 | 863 | 98.6 | 187 | 22 AAEL0345 | Human interferon b |
| 25 | 863 | 98.6 | 187 | 22 AAB49776 | Human interferon-b |
| 26 | 863 | 98.6 | 399 | 21 AAY70867 | IFNAR2/IFN-beta co |
| 27 | 863 | 98.6 | 415 | 20 AAY25371 | Sequence between t |
| 28 | 862 | 98.5 | 166 | 7 AAP60687 | Human interferon b |
| 29 | 860 | 98.3 | 166 | 22 AAU00070 | Human interferon b |
| 30 | 860 | 98.3 | 166 | 22 AAU00072 | Human interferon b |
| 31 | 860 | 98.3 | 166 | 22 AAU00075 | Human interferon b |
| 32 | 860 | 98.3 | 166 | 22 AAU00083 | Human interferon b |
| 33 | 860 | 98.3 | 166 | 22 AAU00085 | Human interferon b |
| 34 | 860 | 98.3 | 166 | 22 AAU00124 | Human interferon b |
| 35 | 860 | 98.3 | 166 | 22 AAU00137 | Human interferon b |
| 36 | 860 | 98.3 | 166 | 22 AAU00143 | Human interferon b |
| 37 | 860 | 98.3 | 166 | 22 AAU00159 | Human interferon b |
| 38 | 860 | 98.3 | 166 | 22 AAU00160 | Human interferon b |
| 39 | 860 | 98.3 | 187 | 3 AAP20049 | Interferon-beta ge |
| 40 | 859 | 98.2 | 166 | 22 AAU00073 | Human interferon b |
| 41 | 859 | 98.2 | 166 | 22 AAU00077 | Human interferon b |
| 42 | 859 | 98.2 | 166 | 22 AAU00078 | Human interferon b |
| 43 | 858 | 98.1 | 165 | 22 AAU00139 | Human interferon b |
| 44 | 858 | 98.1 | 166 | 6 AAP50197 | Modified human int |
| 45 | 858 | 98.1 | 166 | 16 AAR82607 | IFN-beta(Phe101). |

ALIGNMENTS

RESULT 1

| | |
|----------|--|
| AAU00119 | AAU00119 standard; Protein; 166 AA. |
| XX | AAU00119; |
| AC | AAU00119; |
| DT | 16-MAY-2001 (first entry) |
| XX | Human interferon beta mutant Q49N/Q51T. |
| DE | Human; interferon beta; antibody; multiple sclerosis; gene therapy; |
| XX | viral infection; viral hepatitis; cancer; breast cancer; inflammation; |
| KW | Crohn's disease; acute myeloid leukaemia; Hodgkin's disease; |
| KW | ulcerative colitis; immunomodulation; mutant; mutein; Q49N/Q51T. |
| XX | Homo sapiens. |
| OS | XX |
| XX | XX |
| FH | Key Location/Qualifiers |
| FT | Misc-difference 49 /note= "Wild-type Gln replaced with Asn" |
| FT | Misc-difference 51 /note= "Wild-type Gln replaced with Thr" |
| XX | XX |
| PN | WO200115736-A2. |
| XX | XX |
| PD | 08-MAR-2001. |
| XX | XX |
| PF | 25-AUG-2000; 2000WO-DK00471. |
| XX | XX |
| PR | 27-AUG-1999; 99DK-0001197. |
| PR | 21-OCT-1999; 99US-0160782. |
| PR | 26-NOV-1999; 99DK-0001691. |
| PR | 07-FEB-2000; 2000DK-0000194. |
| PR | 07-MAR-2000; 2000DK-0000363. |

PT Multi-class hybrid interferon poly:peptide(s) - with restricted
 XX antiviral and cell growth regulatory activities
 PS
 XX Example; Fig 5; 61pp; English.
 XX
 CC The inventors claim a multiclass hybrid interferon polypeptide and a
 CC DNA unit having a nucleotide sequence which encodes it. Pref. the
 CC AA sequence consists of alpha and beta interferons. Pref. IF1 is
 CC (i) the 1-73 AA seq. of HuIFN-alpha-1 (and IF2 is the 74-166 AA seq.
 CC of HuIFN-beta-1) (see AAN30155, AAP30222); or (ii) the 1-41 AA seq. of
 CC HuIFN-alpha-61A (and IF2 is the 43-166 AA seq. of HuIFN-beta-1) (see
 CC AAN30160, AAP30227). Alternatively IF1 is the amino terminal end of a
 CC beta-IF and IF2 is the carboxy terminal of an alpha-IF (esp. the
 CC 1-73 seq. of HuIFN-beta-1 and the 74-167 seq. of HuIFN-alpha-1
 CC resp.) (see AAN30156, AAP30223). In the examples plasmids pGW5 and
 CC pDM101/trp/beta-1 and p-alpha-61A were used (see AAN30151, AAN30152,
 CC AAN30157). HinfI was used to digest the DNA sequences in the region
 CC of significant handicaps (see AAN30153, AAN30154, AAN30158, AAN30159),
 CC and the restriction fragments were ligated to form hybrid DNA.
 XX
 SQ Sequence 166 AA;

Query Match 98.6%; Score 863; DB 4; Length 166;
 Best Local Similarity 98.8%; Pred. No. 8.2e-70;
 Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDPPEIKQLQNFKEDAALTY 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 msynllgflqrssnfqcqkllwqlngrleyclkdrrmndfpeekqlqfkedaaltly 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 EMLQNIFAIFRQDSSSTGNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 emlqnifairqdsstgnetivenllanvyhqnihlktvleeklekedftrgklmsl 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 HLKRYGGRILHYLKAKEYSHCAWTIVRVETLRNFYFINRLTCYLRN 166
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 hlkrvgrilhyllakeyshcawtivrveillrnfyfinrltgyln 166
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 5
 AAP50262
 ID AAP50262 standard; Protein; 166 AA.
 XX
 AC AAP50262;
 XX
 DT 20-NOV-1991 (first entry)
 XX
 DE Sequence encoded by the sequence between the EcoRI site and the
 DE XhoII site of p-beta-1-trp.
 XX
 KW Expression vector; trp promoter-operator; transformed bacteria.
 XX
 PN US4499188-A.
 XX
 PD 12-FEB-1985.
 XX
 PF 05-MAY-1982; 82US-0375098.
 XX
 PR 05-MAY-1982; 82US-0375098.
 PR 23-JAN-1984; 84CA-0445883.
 XX
 PA (CETU-) CETUS CORP.
 PA (CETU) CETUS CORP.
 XX
 PI Konrad MW, Mark DF;
 XX
 DR WPI; 1985-055962/09.
 DR N-PSDB; AAN50289.
 XX
 PT Polypeptide, esp. interferon, prodn. by transformed bacteria -
 PT cultured in presence of a repressor which is consumed during
 PT growth

XX Example; Fig 5; 12pp; English.
 XX
 CC The inventors claim a process for the prodn. of heterologous
 CC polypeptide by transformed bacteria. The pref. promoter-operator is
 CC trp which controls expression of structural genes encoding
 CC polypeptides of a synthetic pathway forming tryptophan, esp. at a
 CC concn. of 5.3T mg/l (T= predetermined turbidity value measured at
 CC 680nm, esp. 10-100). The transformed bacteria are esp. E.coli contg.
 CC the plasmid p-beta-1-trp. Example 1 concerns the construction of
 CC plasmid p-beta-1-trp for the direct expression of IFN-beta under the
 CC control of trp promoter-operator.
 XX
 SQ Sequence 166 AA;

Query Match 98.6%; Score 863; DB 6; Length 166;
 Best Local Similarity 98.8%; Pred. No. 8.2e-70;
 Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDPPEIKQLQNFKEDAALTY 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 msynllgflqrssnfqcqkllwqlngrleyclkdrrmndfpeekqlqfkedaaltly 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 EMLQNIFAIFRQDSSSTGNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 emlqnifairqdsstgnetivenllanvyhqnihlktvleeklekedftrgklmsl 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 HLKRYGGRILHYLKAKEYSHCAWTIVRVETLRNFYFINRLTCYLRN 166
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 hlkrvgrilhyllakeyshcawtivrveillrnfyfinrltgyln 166
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 6
 AAP50279
 ID AAP50279 standard; protein; 166 AA.
 XX
 AC AAP50279;
 XX
 DT 09-DEC-1991 (first entry)
 XX
 DE Protein sequence encoding synthetic interferon-beta gene.
 DE
 KW Interferon-beta; virucide; antitumor; immunostimulant.
 XX
 OS Synthetic.
 XX
 PN EP131816-A.
 XX
 PD 23-JAN-1985.
 XX
 PF 28-JUN-1984; 84EP-0107498.
 XX
 PR 01-JUL-1983; 83GB-0017880.
 XX
 PA (SEAR) SEARLE G D & CO.
 XX
 PI Bell LD, Boseley PG, Smith JC, Houghton M;
 XX
 DR WPI; 1985-020165/04.
 DR N-PSDB; AAN50306.
 XX
 PT New modified beta-interferon(s) - useful as antiviral,
 PT anti-neoplastic and immuno-modulatory agents.
 XX
 PS Disclosure; Fig 20; 96pp; English.
 XX
 CC The sequence encodes a synthetic interferon-beta which has
 CC increased biological activity compared to natural IFN-beta, and
 CC which is more effective in the treatment of viral or neoplastic
 CC diseases, or immunosuppressed or immunodeficient conditions.
 XX
 SQ Sequence 166 AA;

Query Match 98.6%; Score 863; DB 6; Length 166;
Best Local Similarity 98.8%; Pred. No. 8.2e-70;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEIKQLONFCKEDAALTY 60
DB 1 msynllgflqrsnfcqkllwqlngrleyclkdrrnmfdipeelkqlqgfkedaalTY 60
QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
DB 61 emlqnifaifrqdsstgwnetivenllanvyhqinhkltvleeklekedftrgklmssl 120
QY 121 HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLRN 166
DB 121 hlkrvygrilhyllkakeyshcawtivrveilrnfynrltgyln 166

RESULT 7
AAP70296
ID AAP61071 standard; Protein; 166 AA.
XX AC AAP61071;
XX DT 28-MAY-1991 (first entry)
XX DE Oxidation resistant mutin of Interferon-Beta.
XX KW IL-2; IFN-Beta; colony stimulating factor; CSF-1; tPA; hGF.
XX FH Key Location/Qualifiers
FT Misc-difference 1..6 /note= "May be N-terminal truncated or absent"
FT Misc-difference 17 /note= "May be any conservative AA"
FT Misc-difference 36 /note= "May be any conservative AA"
FT Misc-difference 62 /note= "May be any conservative AA"
FT Misc-difference 117 /note= "May be any conservative AA"
FT Misc-difference 117 /note= "May be any conservative AA"
XX AU8652451-A.
XX PD 31-JUL-1986.
XX PF 17-JAN-1986; 86AU-0052451.
XX PR 17-DEC-1985; 85US-0810656.
XX PR 18-JAN-1985; 85US-0692596.
XX PR 05-NOV-1986; 86AU-0064846.
XX PR 05-AUG-1986; 86US-0893186.
XX (CETU) CETUS CORP.
XX KOths KE, Halenbeck RF, Innis MA;
XX WPI; 1986-239075/37.
XX Oxidn. resistant mutin(s) - prepd. by replacing
XX oxidn.-susceptible methionine with conservative aminoacid
XX Claim 5; Page 50; 50pp; English.
XX Modified peptide has residues susceptible to chloramine T and
XX peroxide oxidation replaced with conservative AAs. Mutin is thus
XX resistant to oxidation. Other proteins which may be similarly
XX rendered resistant include tissue plasminogen activator, colony
XX stimulating factor and human growth factor.
XX Sequence 166 AA;

Query Match 98.6%; Score 863; DB 7; Length 166;
Best Local Similarity 98.8%; Pred. No. 8.2e-70;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEIKQLONFCKEDAALTY 60
DB 1 msynllgflqrsnfcqkllwqlngrleyclkdrrnmfdipeelkqlqgfkedaalTY 60
QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
DB 61 emlqnifaifrqdsstgwnetivenllanvyhqinhkltvleeklekedftrgklmssl 120
QY 121 HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLRN 166
DB 121 hlkrvygrilhyllkakeyshcawtivrveilrnfynrltgyln 166

RESULT 8
AAP70296
ID AAP70296 standard; protein; 166 AA.
XX AC AAP70296;
XX DT 07-JUN-1991 (first entry)
XX DE Sequence of interferon-beta.
XX KW Antiviral; antiproliferative agent.
XX OS Homo sapiens.
XX PN EP237019-A.
XX PD 16-SEP-1987.
XX PF 10-MAR-1987; 87EP-0103406.
XX PR 14-MAR-1986; 86JP-0054650.
XX PR 26-DEC-1986; 86JP-0308693.
XX (TORA) TORAY IND INC.
XX Tanaka T, Kawano G, Sawada R;
XX WPI; 1987-258309/37.
XX Conjugates of Interferon(s)-beta and-gamma - useful as antivirals
XX and anti-cell proliferatives with broader spectrum of activity
XX and obt'd. economically by recombinant DNA procedures
XX Claim 7; p35; 52pp; English.
XX The inventors claim an interferon conjugate wherein a C-terminal of
XX the region exhibiting biological activities of interferon-beta has
XX been linked to an N-terminal of the region exhibiting biological
XX activities of interferon-gamma. The antiviral activity of the
XX conjugate was tested using FL cells-sindbis virus system according
XX to the CPE 50 inhibition method. Antiviral activity ranged from
XX 200 U/ml to 18500 U/ml.
XX Sequence 166 AA;

Query Match 98.6%; Score 863; DB 8; Length 166;
Best Local Similarity 98.8%; Pred. No. 8.2e-70;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEIKQLONFCKEDAALTY 60
DB 1 msynllgflqrsnfcqkllwqlngrleyclkdrrnmfdipeelkqlqgfkedaalTY 60
QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120

Db 61 emlqnifalfrqdsstgwnetivlenllanyhghnlhktvleeklekedftrgklmssl 120
QY 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
Db 121 hlkrvggrilhyllkakeyshcawtivrveilrnfynrltgyln 166
RESULT 9
AAW81774
ID AAW81774 standard; protein; 166 AA.
XX AAW81774;
AC AAW81774;
DT 29-JAN-1999 (first entry)
DE Human native interferon-beta protein.
XX Interferon-Beta; variant; human; medicament; treatment; screening;
KW multiple sclerosis; measurement; water soluble.
XX Homo sapiens.
OS DE19717864-A1.
PN 29-OCT-1998.
PD 23-APR-1997; 97DE-1017864.
PF 23-APR-1997; 97DE-1017864.
PR (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
PA Otto B, Schneider-Fresenius C, Waschuetza G;
PI WPI; 1998-569784/49.
DR New mutated recombinant human interferon-beta protein contains
PT hydroxylic amino acid substitutions to improve water solubility -
PT used e.g. in vitro screening assays, to measure interferon levels
PT and to treat multiple sclerosis
XX Disclosure; Fig 1; 18pp; German.
XX This sequence represents a native human recombinant interferon-beta
CC protein which is mutated into an amino acid having at least one hydroxy
CC group substituted for at least one of Leu5, Phe8, Phe15, Leu47, Phe50,
CC Leu106, Phe111, Leu116, Leu120 and Phe156. Such mutants can be used in
CC medicaments e.g. for treating multiple sclerosis, for in vitro screening
CC assays and for measurement of interferon levels. The mutated protein is
CC more water-soluble than recombinant wild-type human interferon-beta.
XX
SQ Sequence 166 AA;
Query Match 98.6%; Score 863; DB 19; Length 166;
Best Local Similarity 98.8%; Pred. No. 8.2e-70;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MSYNLLGFLQRSSNFQCKLLWOLNGRLLEYCLKDRMNFDPPEETKOLQNFKEADAALTY 60
Db 1 msynllgflqrssnfqckllwqlngrlleyclckdrmfndipeelkqlqgfkedaaltly 60
QY 61 EMLQNIFAIPRODSSSTGWNETIVENLLANYVHQLNKTVELEKEDFTRGKLMSSL 120
Db 61 emlqnifalfrqdsstgwnetivlenllanyhghnlhktvleeklekedftrgklmssl 120
QY 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
Db 121 hlkrvggrilhyllkakeyshcawtivrveilrnfynrltgyln 166

RESULT 10

AAE10346
ID AAE10346 standard; Protein; 166 AA.
XX AAE10346;
AC AAE10346;
DT 10-DEC-2001 (first entry)
XX Mature human beta-interferon.
DE Human; beta-interferon; INF-beta; immune disease; demyelinating disease;
KW sub-acute sclerosing panencephalomyelitis; SSPE; multiple sclerosis;
KW metachromatic leukodystrophy; Guillain-Barre syndrome;
KW autoimmune disease.
XX Homo sapiens.
OS Key Location/Qualifiers
FH Misc-difference 162
FT /note= "Encoded by CGT"
XX EP1133997-A2.
PN 19-SEP-2001.
PD 20-FEB-2001; 2001EP-0103580.
PF 23-FEB-2000; 2000EP-0440053.
PR 07-NOV-2000; 2000US-0246089.
PA (TRGE) TRANSGENE SA.
XX Braun S;
PI WPI; 2001-572706/65.
DR N-PSDB; AAD17506.
XX Use of nucleic acid for the treatment of immune diseases such as
PT multiple sclerosis -
PS Claim 9; Page 15; 21pp; English.
XX The invention relates to use of nucleic acids expressing human
CC beta-interferon (INF-beta) for the treatment of immune diseases such as
CC demyelinating disease (e.g. sub-acute sclerosing panencephalomyelitis
CC (SSPE), metachromatic leukodystrophy, Guillain-Barre syndrome) and
CC autoimmune disease (e.g. multiple sclerosis). The expression of the
CC beta-interferon results in the improvement of the clinical status of
CC the treated mammal, thus avoiding the use of recombinant polypeptide.
CC The nucleic acid is therefore compatible with the quality of life of the
CC patients. The present sequence is mature human beta-interferon.
XX
SQ Sequence 166 AA;
Query Match 98.6%; Score 863; DB 22; Length 166;
Best Local Similarity 98.8%; Pred. No. 8.2e-70;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MSYNLLGFLQRSSNFQCKLLWOLNGRLLEYCLKDRMNFDPPEETKOLQNFKEADAALTY 60
Db 1 msynllgflqrssnfqckllwqlngrlleyclckdrmfndipeelkqlqgfkedaaltly 60
QY 61 EMLQNIFAIPRODSSSTGWNETIVENLLANYVHQLNKTVELEKEDFTRGKLMSSL 120
Db 61 emlqnifalfrqdsstgwnetivlenllanyhghnlhktvleeklekedftrgklmssl 120
QY 121 HLKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
Db 121 hlkrvggrilhyllkakeyshcawtivrveilrnfynrltgyln 166
RESULT 11
AAE11979

| | | |
|-----------|---|----------------------------|
| ID | AAE11979 | standard; Protein; 166 AA. |
| XX | | |
| AC | AAE11979; | |
| XX | | |
| DT | 18-DEC-2001 | (first entry) |
| XX | | |
| DE | Human wild-type interferon (IFN) beta. | |
| XX | | |
| KW | Human; interferon-gamma; IFNG; interferon-beta; interferon alpha; FSH; | |
| KW | follicle stimulating hormone; granulocyte colony stimulating factor; | |
| KW | G-CSF; interleukin 10; IL-10; medicament; pulmonary administration; | |
| KW | circulatory administration. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PN | WO200168141-A2. | |
| XX | | |
| PD | 20-SEP-2001. | |
| XX | | |
| PF | 16-MAR-2001; 2001WO-DK00182. | |
| XX | | |
| PR | 17-MAR-2000; 2000DK-0000447. | |
| XX | | |
| PR | 20-MAR-2000; 2000US-150844P. | |
| XX | | |
| PR | 25-AUG-2000; 2000WO-DK00471. | |
| XX | | |
| PR | 13-NOV-2000; 2000WO-DK00631. | |
| XX | | |
| PA | (MAXY-) MAXYGEN APS. | |
| XX | | |
| PI | Hansen CK; | |
| XX | | |
| DR | WPI; 2001-616274/71. | |
| XX | | |
| PT | Dispersions of particles for administration to the lung and circulatory | |
| XX | system by inhalation, e.g. from a nebulizer - | |
| XX | | |
| PS | Claim 22; Page 136; 139pp; English. | |
| XX | | |
| CC | The present invention relates to novel dispersions of a conjugate | |
| CC | comprising at least one non-polypeptide moiety covalently attached | |
| CC | to a polypeptide variant, wherein the amino acid sequence of the | |
| CC | polypeptide variant differs from that of the corresponding wild-type | |
| CC | human polypeptide in that at least 1 residue comprising an attachment | |
| CC | group for the non-polypeptide group has been introduced and/or removed. | |
| CC | The wild-type human polypeptide is selected from the group consisting | |
| CC | of interferon-gamma (IFNG), interferon-beta, interferon alpha, follicle | |
| CC | stimulating hormone (FSH), interleukin 10 (L-10) and granulocyte colony | |
| CC | stimulating factor (G-CSF). The dispersion is used for the preparation | |
| CC | of a medicament for pulmonary and/or circulatory administration. The | |
| CC | present sequence is human wild type interferon (IFN) beta. | |
| XX | | |
| SQ | Sequence 166 AA; | |
| | | |
| | Query Match 98.6%; Score 863; DB 22; Length 166; | |
| | Best Local Similarity 98.8%; Pred. No. 8.2e-70; | |
| | Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps | |
| QY | 1 MSYNLLGFLORSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEEIKQLONFTKEDAAITY 60 | |
| DB | | |
| | 1 msynllgflgrssnfqckllwqlngrleyclkrmndfpeeklqgqkedaaity 60 | |
| QY | 61 EMLQNIQFAIRQDSSSTGWNETIVENLLANVYHQINHLKTVEEKLEKEDFTCKLMSSL 120 | |
| DB | | |
| | 61 emlqnifalfrqdasstgwnetivenllanvyhqnhlktvleeklekedftrgklmssl 120 | |
| QY | 121 HLKRYYGRIHLHYLKAKEYSHCAWTVRVEILRNFFYNRLTGYLRN 166 | |
| DB | | |
| | 121 hlkryygrilhyllkakeyshcawtivrveilrnfynrlngcylrn 166 | |
| RESULT 12 | | |
| AAU00038 | | |
| ID | AAU00038 | standard; Protein; 166 AA. |

XX AAU00038;
AC 16-MAY-2001 (first entry)
XX Human interferon beta.
DT
XX
DE
XX Human; interferon beta; antibody; multiple sclerosis; gene therapy;
KW viral infection; viral hepatitis; cancer; breast cancer; inflammation;
KW Crohn's disease; acute myeloid leukaemia; Hodgkin's disease;
KW ulcerative colitis; immunomodulation.
XX
XX Homo sapiens.
OS
XX WO200115736-A2.
PN
XX 08-MAR-2001.
PD
XX 25-AUG-2000; 2000WO-DK00471.
PF
XX 27-AUG-1999; 99DK-0001197.
PR 21-OCT-1999; 99US-0160782.
PR 26-NOV-1999; 99DK-0001691.
PR 07-FEB-2000; 2000DK-0000194.
PR 07-MAR-2000; 2000DK-0000363.
PR 14-APR-2000; 2000DK-0000642.
XX
XX (MAXY-) MAXYGEN APS.
PA
XX Pedersen AH, Schambye HT, Andersen KV, Bornaes C, Rasmussen PB;
PI WPI; 2001-218485/22.
PI N-PSDB; AAS00067.
XX
XX A conjugate exhibiting interferon beta activity useful for treating
PT multiple sclerosis comprises a non-polypeptide group covalently
PT attached to an interferon beta polypeptide -
PT
XX
XX Example 1; Page 99-100; 108pp; English.
PS
XX
XX The sequence is Human interferon beta. Conjugates of the invention
CC exhibiting interferon beta activity comprise at least one first
CC non-polypeptide group covalently attached to an interferon beta
CC polypeptide, the amino acid sequence of which differs from wild-type
CC human interferon beta in at least one introduced and at least one removed
CC amino acid residue comprising an attachment group for the first
CC non-polypeptide group. The invention also concerns reducing the
CC immunogenicity and/or increasing functional *in vivo* half-life and/or
CC serum half-life of an interferon beta polypeptide comprising introducing
CC an amino acid residue constituting an attachment group for a first
CC non-polypeptide group into a position exposed at the surface of the
CC protein that does not contain such a group and removing an amino acid
CC residue constituting an attachment group for a first non-polypeptide
CC group and subjecting the modified peptide to conjugation with the
CC non-polypeptide group. The conjugate and a cell culture expressing the
CC mutated polypeptides are useful in the treatment of disease, especially
CC multiple sclerosis, and for treating mammals having circulating
CC antibodies against interferon beta *in vivo*. DNA encoding the mutated
CC proteins may be used for gene therapy. The DNA and proteins can also be
CC used to treat viral infections (e.g. viral hepatitis), cancer (e.g.
CC breast cancer), inflammation, Crohn's disease, acute myeloid leukaemia,
CC Hodgkin's disease and ulcerative colitis and for immunomodulation.
XX
XX Sequence 166 AA;
SQ

Query Match 98.6%; Score 863; DB 22; Length 166;
Best Local Similarity 98.8%; Pred. No. 8.2e-70;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSYNLLGLFQRSNFFQCKLWLQNLGRLEYCLKDRNFDIPEETIKQLQNFKEDAAALTY 60
Db 1 msvnlglfqrssnffgckllwlqnlgrllevclkdrrmfdipeetkqlgqfkdadaaltiv 60

QY 61 EMLQNIFAIPRODSSSTGNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
 Db 61 emlqnifairqdsstgnetivenllanvyhqinhkvtiveeklekedftrgklmssl 120
 QY 121 HLKRYGGRILHYLKAKEYSHCAWTIVRVEILRNPFYFINRLTGYLRN 166
 Db 121 hlkrvgygrilhyikakeyshcawtivrveilrnfynfynrltgyln 166

RESULT 13
 AAU00074
 ID AAU00074 standard; Protein; 166 AA.
 AC AAU00074;
 XX 16-MAY-2001 (first entry)
 XX Human interferon beta mutant Q49K.
 XX Human; interferon beta; antibody; multiple sclerosis; gene therapy;
 KW viral infection; viral hepatitis; cancer; breast cancer; inflammation;
 KW Crohn's disease; acute myeloid leukaemia; Hodgkin's disease;
 KW ulcerative colitis; immunomodulation; mutant; mutein; Q49K.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 49 /note= "Wild-type Gln replaced with Lys"
 FT
 XX
 PN WO200115736-A2.
 XX
 XX 08-MAR-2001.
 XX
 XX 25-AUG-2000; 2000WO-DK00471.
 XX
 XX 27-AUG-1999; 99DK-0001197.
 PR 21-OCT-1999; 99US-0160782.
 PR 26-NOV-1999; 99DK-0001691.
 PR 07-FEB-2000; 2000DK-0000194.
 PR 07-MAR-2000; 2000DK-0000363.
 PR 14-APR-2000; 2000DK-0000642.
 XX
 PA (MAXY-) MAXYGEN APS.
 XX
 XX Pedersen AH, Schambye HT, Andersen KV, Bornaes C, Rasmussen PB;
 PI WPI; 2001-218488/22.
 XX
 XX A conjugate exhibiting interferon beta activity useful for treating
 PT multiple sclerosis comprises a non-polypeptide group covalently
 PT attached to an interferon beta polypeptide -
 XX
 XX Claim 11; Page - ; 108pp; English.
 PS
 XX The sequence represents Human interferon beta mutant Q49K.
 CC Conjugates of the invention exhibiting interferon beta activity
 CC comprise at least one first non-polypeptide group covalently attached
 CC to an interferon beta polypeptide, the amino acid sequence of which
 CC differs from wild-type human interferon beta in at least one introduced
 CC and at least one removed amino acid residue comprising an attachment
 CC group for the first non-polypeptide group. The invention also concerns
 CC reducing the immunogenicity and/or increasing functional in vivo
 CC half-life and/or serum half-life of an interferon beta polypeptide
 CC comprising introducing an amino acid residue constituting an attachment
 CC group for a first non-polypeptide group into a position exposed at the
 CC surface of the protein that does not contain such a group and removing
 CC an amino acid residue constituting an attachment group for a first
 CC non-polypeptide group and subjecting the modified peptide to conjugation
 CC with the non-polypeptide group. The conjugate and a cell culture
 CC expressing the mutated polypeptides are useful in the treatment of
 CC disease, especially multiple sclerosis, and for treating mammals having

CC circulating antibodies against interferon beta 1a or 1b. DNA encoding the
 CC mutated proteins may be used for gene therapy. The DNA and proteins can
 CC also be used to treat viral infections (e.g. viral hepatitis), cancer
 CC (e.g. breast cancer), inflammation, Crohn's disease, acute myeloid
 CC leukaemia, Hodgkin's disease and ulcerative colitis and for
 CC immunomodulation.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the human interferon beta sequence given in AAU00038.
 XX
 SQ Sequence 166 AA;
 Query Match 98.6%; Score 863; DB 22; Length 166;
 Best Local Similarity 98.8%; Pred. No. 8.2e-70;
 Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MSYNLLGFLQSSNFQCOKLLWOLNGRLCYCLKDRMNFDPETIKOLQNTKEDAAALTIY 60
 Db 1 msynllgflqssnfgcqkllwqlngfleyclkdrmfdpetkqlqkfgedaaltiy 60
 QY 61 EMLQNIFAIPRODSSSTGNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
 Db 61 emlqnifairqdsstgnetivenllanvyhqinhkvtiveeklekedftrgklmssl 120
 QY 121 HLKRYGGRILHYLKAKEYSHCAWTIVRVEILRNPFYFINRLTGYLRN 166
 Db 121 hlkrvgygrilhyikakeyshcawtivrveilrnfynfynrltgyln 166

RESULT 14
 AAB49356
 ID AAB49356 standard; Protein; 166 AA.
 XX
 AC AAB49356;
 XX
 DT 07-MAR-2001 (first entry)
 XX
 XX Human INF-beta A-chain.
 DE
 DE Interferon-beta activity; multiple sclerosis; cancer; viral infection;
 KW analogue.
 KW
 XX Homo sapiens.
 OS
 XX WO2000068387-A2.
 PN
 XX 16-NOV-2000.
 PD
 XX 12-MAY-2000; 2000WO-US13216.
 PF
 XX 12-MAY-1999; 99US-0133785.
 PR
 XX (XENC-) XENCOR INC.
 PA
 XX Bentzien J;
 PI
 XX WPI; 2001-007398/01.
 DR
 XX Novel interferon-beta activity (IBa) proteins which have greater
 PT stability than interferon-beta (IFN-beta) useful for the treatment of
 PT IFN-beta related disorders such as multiple sclerosis -
 XX
 PS Disclosure; Fig 1A; 109pp; English.
 XX The present invention provides proteins which have interferon-beta
 CC (IFN-beta) activity. These analogues are produced so that they are less
 CC than 97% identical to human IFN-beta. They are useful in the treatment of
 CC multiple sclerosis, cancer, particularly osteosarcoma, basal cell
 CC carcinoma, cervical dysplasia, glioma, acute myeloid leukaemia, multiple
 CC myeloma, Hodgkin's disease, melanoma, and renal, liver and breast
 CC cancers, viral infections, including those caused by hepatitis viruses,
 CC herpes viruses and papilloma viruses, viral encephalitis, cytomegalovirus
 CC pneumonia and prophylaxis of rhinovirus, idiopathic pulmonary fibrosis

CC and inflammatory diseases.

| AA | Sequence | 166 AA; |
|----|----------|---------|
| SQ | | |

Query Match 98.6%; Score 863; DB 22; Length 166;

Best Local Similarity 98.8%; Pred. No. 8.2e-70;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 MSYNLLGFQRRSSNFQCQKLLWQLNGRLEYCLKDRMNFDP E E I K Q L Q n F t K E D A A L T I Y 60

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Db 1 msynllgflgrssnfcqkllwqlngrleyclkdrrnfdipeelkqlqfqkedaaltly 60

0v 61 FMIONTEATEBODSSSTCWNETIVENILANLUYHOYNHIKTVI EEKI EKFDEETDCKI MESSI 120

QY 61 EMLQJNIFAFRQDSSSIGWNETIIVENLLANVIHQJNHLKTVLEEKLEKED

Db 61 emlqn1fa1frqdsstgwnetivenllanvyhqn1h1ktvleekleked

RESULT 15

AAB49357

ID AAB49357 standard; Protein; 166 AA.

AC AAB49357;

07-MAR-2001 (first entry)

Human INF-beta B-chain.

AA Interferon-beta activity; multiple sclerosis; cancer; viral infection;
KW Interferon-beta activity; multiple sclerosis; cancer; viral infection;
KW analogue.

OS Homo sapiens.

AA
PN
WO200068387-A2.XX
PD
16-NOV-2000.

12-MAY-2000: 2000WO-US13216.

XX
PR 12-MAY-1999: 99MS-0133785.

PA (XENC-) XENCOR INC.

XX
PI Bentzien J:

XX
DR WPI: 2001-007398/01.

Novel interferon-beta activity (IbA) proteins which have greater stability than interferon-beta (IFN-beta) useful for the treatment of IFN-beta related disorders such as multiple sclerosis -

PS Example 1; Fig 1B; 109pp; English.

The present invention provides proteins which have interferon-beta (IFN-beta) activity. These analogues are produced so that they are less than 97% identical to human IFN-beta. They are useful in the treatment of multiple sclerosis, cancer, particularly osteosarcoma, basal cell carcinoma, cervical dysplasia, glioma, acute myeloid leukaemia, multiple myeloma, Hodgkin's disease, melanoma, and renal, liver and breast cancers, viral infections, including those caused by hepatitis viruses, herpes viruses and papilloma viruses, viral encephalitis, cytomegalovirus pneumonia and prophylaxis of rhinovirus, idiopathic pulmonary fibrosis and inflammatory diseases.

| AA | Sequence | 166 AA; |
|----|----------|---------|
| SQ | | |

Query Match 98.68; Score 863; DB 22; Length 166;

Best Local Similarity 98.88; Pred. No. 8.2e-70;

| | | | | | | | | | |
|---------|------|--------------|----|------------|----|--------|----|------|----|
| Matches | 164; | Conservative | 0; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
|---------|------|--------------|----|------------|----|--------|----|------|----|

QY 1 MSYNLLGFLQSSNFQCOKLLWLQNGRLEYCLKDRMNFDIPEEIKOLONFtKEDAALTY 60

| DATE | DESCRIPTION | AMOUNT | BALANCE |
|----------|-----------------|--------|----------|
| 1/1/20 | OPENING BALANCE | | 100.00 |
| 1/15/20 | PAYROLL | 50.00 | 50.00 |
| 1/20/20 | RENT | 25.00 | 25.00 |
| 1/25/20 | UTILITIES | 15.00 | 10.00 |
| 1/30/20 | SALES | 75.00 | 85.00 |
| 2/5/20 | PAYROLL | 50.00 | 35.00 |
| 2/10/20 | RENT | 25.00 | 10.00 |
| 2/15/20 | UTILITIES | 15.00 | (5.00) |
| 2/20/20 | SALES | 75.00 | 70.00 |
| 2/25/20 | PAYROLL | 50.00 | 20.00 |
| 2/28/20 | RENT | 25.00 | (5.00) |
| 3/5/20 | UTILITIES | 15.00 | (20.00) |
| 3/10/20 | SALES | 75.00 | 55.00 |
| 3/15/20 | PAYROLL | 50.00 | 5.00 |
| 3/20/20 | RENT | 25.00 | (20.00) |
| 3/25/20 | UTILITIES | 15.00 | (35.00) |
| 3/30/20 | SALES | 75.00 | 40.00 |
| 4/5/20 | PAYROLL | 50.00 | (10.00) |
| 4/10/20 | RENT | 25.00 | (35.00) |
| 4/15/20 | UTILITIES | 15.00 | (50.00) |
| 4/20/20 | SALES | 75.00 | (25.00) |
| 4/25/20 | PAYROLL | 50.00 | (75.00) |
| 4/30/20 | RENT | 25.00 | (100.00) |
| 5/5/20 | UTILITIES | 15.00 | (115.00) |
| 5/10/20 | SALES | 75.00 | (40.00) |
| 5/15/20 | PAYROLL | 50.00 | (90.00) |
| 5/20/20 | RENT | 25.00 | (115.00) |
| 5/25/20 | UTILITIES | 15.00 | (130.00) |
| 5/30/20 | SALES | 75.00 | (55.00) |
| 6/5/20 | PAYROLL | 50.00 | (105.00) |
| 6/10/20 | RENT | 25.00 | (130.00) |
| 6/15/20 | UTILITIES | 15.00 | (145.00) |
| 6/20/20 | SALES | 75.00 | (70.00) |
| 6/25/20 | PAYROLL | 50.00 | (120.00) |
| 6/30/20 | RENT | 25.00 | (145.00) |
| 7/5/20 | UTILITIES | 15.00 | (160.00) |
| 7/10/20 | SALES | 75.00 | (85.00) |
| 7/15/20 | PAYROLL | 50.00 | (135.00) |
| 7/20/20 | RENT | 25.00 | (160.00) |
| 7/25/20 | UTILITIES | 15.00 | (175.00) |
| 7/30/20 | SALES | 75.00 | (100.00) |
| 8/5/20 | PAYROLL | 50.00 | (150.00) |
| 8/10/20 | RENT | 25.00 | (175.00) |
| 8/15/20 | UTILITIES | 15.00 | (190.00) |
| 8/20/20 | SALES | 75.00 | (115.00) |
| 8/25/20 | PAYROLL | 50.00 | (165.00) |
| 8/30/20 | RENT | 25.00 | (190.00) |
| 9/5/20 | UTILITIES | 15.00 | (205.00) |
| 9/10/20 | SALES | 75.00 | (130.00) |
| 9/15/20 | PAYROLL | 50.00 | (180.00) |
| 9/20/20 | RENT | 25.00 | (205.00) |
| 9/25/20 | UTILITIES | 15.00 | (220.00) |
| 9/30/20 | SALES | 75.00 | (145.00) |
| 10/5/20 | PAYROLL | 50.00 | (195.00) |
| 10/10/20 | RENT | 25.00 | (220.00) |
| 10/15/20 | UTILITIES | 15.00 | (235.00) |
| 10/20/20 | SALES | 75.00 | (160.00) |
| 10/25/20 | PAYROLL | 50.00 | (210.00) |
| 10/30/20 | RENT | 25.00 | (235.00) |
| 11/5/20 | UTILITIES | 15.00 | (250.00) |
| 11/10/20 | SALES | 75.00 | (175.00) |
| 11/15/20 | PAYROLL | 50.00 | (225.00) |
| 11/20/20 | RENT | 25.00 | (250.00) |
| 11/25/20 | UTILITIES | 15.00 | (265.00) |
| 11/30/20 | SALES | 75.00 | (190.00) |
| 12/5/20 | PAYROLL | 50.00 | (240.00) |
| 12/10/20 | RENT | 25.00 | (265.00) |
| 12/15/20 | UTILITIES | 15.00 | (280.00) |
| 12/20/20 | SALES | 75.00 | (205.00) |
| 12/25/20 | PAYROLL | 50.00 | (255.00) |
| 12/30/20 | RENT | 25.00 | (280.00) |
| 1/5/21 | UTILITIES | 15.00 | (295.00) |
| 1/10/21 | SALES | 75.00 | (220.00) |
| 1/15/21 | PAYROLL | 50.00 | (270.00) |
| 1/20/21 | RENT | 25.00 | (295.00) |
| 1/25/21 | UTILITIES | 15.00 | (310.00) |
| 1/30/21 | SALES | 75.00 | (235.00) |
| 2/5/21 | PAYROLL | 50.00 | (285.00) |
| 2/10/21 | RENT | 25.00 | (310.00) |
| 2/15/21 | UTILITIES | 15.00 | (325.00 |

Db 1 msynllgflqrssnfcqkllwqlngrleyclkdrrnfdipeikqlqqfkedaaltiy 60

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61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKED QY

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Search completed: July 29, 2002, 15:42:54

Job time: 230 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2002, 15:40:29 ; Search time 28.3 Seconds
(without alignments)
563.634 Million cell updates/sec

Title: SEQ2-49N-51S
Perfect score: 874
Sequence: 1 MSYNLLGLQSSNFQCKL.....RVEILRNFYFINRLTGYLRN 166
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 864 | 98.9 | 187 | 1 IVHUB1 | interferon beta-1 |
| 2 | 482.5 | 55.2 | 186 | 1 IVBOB2 | interferon beta-2 |
| 3 | 477.5 | 54.6 | 186 | 1 IVHOBI | interferon beta-1 |
| 4 | 451.5 | 51.7 | 186 | 1 IVBOB3 | interferon beta-3 |
| 5 | 430.5 | 49.3 | 186 | 1 IVBOB1 | interferon beta-1 |
| 6 | 336.5 | 38.5 | 182 | 1 IVMSB | interferon beta pr |
| 7 | 328.5 | 37.6 | 184 | 2 JC5424 | interferon beta pr |
| 8 | 284 | 32.5 | 195 | 1 IVHO22 | interferon alpha-I |
| 9 | 263 | 30.1 | 195 | 1 IVHO21 | interferon alpha-I |
| 10 | 257 | 29.4 | 184 | 1 IVHOA4 | interferon alpha-I |
| 11 | 257 | 29.4 | 184 | 1 IVHOA3 | interferon alpha-I |
| 12 | 257 | 29.4 | 184 | 1 IVHOA1 | interferon alpha-I |
| 13 | 253 | 28.9 | 184 | 1 IVHOA2 | interferon alpha-I |
| 14 | 250.5 | 28.7 | 189 | 1 IVHU16 | interferon alpha-I |
| 15 | 250.5 | 28.7 | 189 | 2 I37584 | interferon alpha-I |
| 16 | 247.5 | 28.3 | 195 | 1 IVBOII | IFN-alpha-N-protei |
| 17 | 245.5 | 28.1 | 165 | 2 I78570 | interferon alpha-I |
| 18 | 245.5 | 28.1 | 172 | 2 A61578 | alpha 2 interferon |
| 19 | 245.5 | 28.1 | 195 | 2 A61455 | trophoblast protei |
| 20 | 244.5 | 28.0 | 188 | 1 IVHUA2 | trophoblast protei |
| 21 | 244 | 27.9 | 195 | 1 IVHUII | interferon alpha-2 |
| 22 | 243.5 | 27.9 | 189 | 1 IVHU4B | interferon omega-1 |
| 23 | 241.5 | 27.6 | 167 | 2 F25843 | interferon alpha-I |
| 24 | 241.5 | 27.6 | 189 | 1 IVHUA7 | interferon alpha-J |
| 25 | 241.5 | 27.6 | 189 | 1 IVHUA0 | interferon alpha-7 |
| 26 | 240.5 | 27.5 | 189 | 2 I53102 | interferon-alpha-J |
| 27 | 240.5 | 27.4 | 189 | 2 I52347 | trophoblast interf |
| 28 | 239.5 | 27.4 | 189 | 2 I52347 | interferon alpha-M |
| 29 | 239.5 | 27.4 | 195 | 2 I47068 | trophoblast protei |

ALIGNMENTS

RESULT 1

IVHUB1

Interferon beta-1 precursor [validated] - human

C;Species: Homo sapiens (man)

C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 08-Dec-2000

C;Accession: A93721; A93887; A91468; A93225; A93706; A93700; A93269; S04479; I56315;

R;Lawn, R.M.; Adelman, J.; Franke, A.E.; Houck, C.M.; Gross, M.; Najarian, R.; Goedde

Nucleic Acids Res. 9, 1045-1052, 1981

A;Title: Human fibroblast interferon gene lacks introns.

A;Reference number: A93721; MUID:81198952

A;Accession: A93721

A;Molecule type: DNA

A;Residues: 1-187 <LAW>

A;Cross-references: GB:V00535; NID:g32639; PIDN:CAA23796.1; PID:g32640

R;Ohno, S.; Taniguchi, T.

Proc. Natl. Acad. Sci. U.S.A. 78, 5305-5309, 1981

A;Title: Structure of a chromosomal gene for human interferon beta.

A;Reference number: A93887

A;Accession: A93887

A;Molecule type: DNA

A;Residues: 1-187 <OHN>

R;Taniguchi, T.; Ohno, S.; Fujii-Kuriyama, Y.; Muramatsu, M.

Gene 10, 11-15, 1980

A;Title: The nucleotide sequence of human fibroblast interferon cDNA.

A;Reference number: A91468; MUID:81005095

A;Accession: A91468

A;Molecule type: mRNA

A;Residues: 1-187 <TAN>

A;Cross-references: GB:V00546; NID:g32735; PIDN:CAA23807.1; PID:g32736

R;Derynck, R.; Content, J.; Declercq, E.; Volckaert, G.; Tavernier, J.; Devos, R.; Fl

Nature 285, 542-547, 1980

A;Title: Isolation and structure of a human fibroblast interferon gene.

A;Reference number: A93225; MUID:80254542

A;Accession: A93225

A;Molecule type: DNA

A;Residues: 1-187 <DER>

A;Cross-references: GB:V00546; NID:g32735; PIDN:CAA23807.1; PID:g32736

R;Houghton, M.; Eaton, M.A.W.; Stewart, A.G.; Smith, J.C.; Doel, S.M.; Cartlin, G.H.;

Nucleic Acids Res. 8, 2885-2894, 1980

A;Title: The complete amino acid sequence of human fibroblast interferon as deduced u

A;Reference number: A93706; MUID:81053720

A;Accession: A93706

A;Molecule type: mRNA

A;Residues: 1-187 <HOU>

A;Cross-references: GB:J00218; GB:K00616; GB:M11029; NID:g184626; PID:g386802

R;Houghton, M.; Stewart, A.G.; Doel, S.M.; Emtage, J.S.; Eaton, M.A.W.; Smith, J.C.;

Nucleic Acids Res. 8, 1913-1931, 1980

A;Title: The amino-terminal sequence of human fibroblast interferon as deduced from r

A;Reference number: A93700; MUID:81053854

A;Accession: A93700

A;Molecule type: mRNA

A;Residues: 1-68 <HO2>

R:Wetzel, R.
Nature 289, 606-607, 1991
A:Title: Assignment of the disulphide bonds of leukocyte interferon.
A:Reference number: A93244; MUID:81123083
A:Contents: annotation; disulfide bond
R:Shepard, H.M.; Leung, D.; Stebbing, N.; Goeddel, D.V.
Nature 294, 563-565, 1991
A:Title: A single amino acid change in IFN-beta-1 abolishes its antiviral activity.
A:Reference number: A93269; MUID:82080683

A:Accession: A93269
A:Molecule type: mRNA
A:Residues: 71-161, 'Y', 163-187 <SIG>
A:Experimental source: variant, clone pF526
A:Note: the loss of Cys-162 (and of the ability to form the essential disulfide bond) in
R:Utsumi, J.; Mizuno, Y.; Hosoi, K.; Okano, K.; Sawada, R.; Kajitani, M.; Sakai, I.; Nae
Eur. J. Biochem. 181, 545-553, 1989
A:Title: Characterization of four different mammalian-cell-derived recombinant human int
A:Reference number: S04479; MUID:89276336
A:Accession: S04479
A>Status: preliminary
A:Molecule type: protein
A:Residues: 22-187 <UTS>
R:May, L.T.; Sehgal, P.B.
J. Interferon Res. 5, 521-526, 1985
A:Title: On the relationship between human interferon alpha-1 and beta-1 genes.
A:Reference number: I56315; MUID:86035565

A:Accession: I56315
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-187 <RES>
A:Cross-references: GB:M28622; NID:g184624; PIDN:AAA36040.1; PID:g184625
C:Genetics:
A:Gene: GDB:IFNB1; IFNB
A:Cross-references: GDB:120522; OMIM:147640
A:Map position: 9p21-9p21
C:Superfamily: Interferon alpha
C:Keywords: antiviral
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-187/Product: interferon beta-1 #status experimental <MAT>
F:52-162/Disulfide bonds: #status predicted

Query Match 98.9%; Score 864; DB 1; Length 187;
Best Local Similarity 98.8%; Pred. No. 3.7e-63;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSYNLLGFLQSSNFQCKLLWQLNGRLVCLKDRMNFDPPEIKQLQNFKEDAAALTYI 60
Db 22 MSYNLLGFLQSSNFQCKLLWQLNGRLVCLKDRMNFDPPEIKQLQNFQKEDAAALTYI 81
Qy 61 EMLQNIFAIPRODSSSTGWNETHVENLLANVYHQINHLKTVLEKLEKEDFTRGKLMSSL 120
Db 82 EMLQNIFAIPRODSSSTGWNETHVENLLANVYHQINHLKTVLEKLEKEDFTRGKLMSSL 141
Qy 121 HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
Db 142 HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 187

RESULT 2
IVBOB2
Interferon beta-2 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 07-Feb-1997
C:Accession: A01840
R:Leung, D.W.; Capon, D.J.; Goeddel, D.V.
Bio/Technology 2, 458-464, 1984
A:Title: The structure and bacterial expression of three distinct bovine interferon-beta
A:Reference number: A90097
A:Accession: A01840
A:Molecule type: DNA
A:Residues: 1-186 <LEU>
C:Superfamily: interferon alpha

C:Keywords: glycoprotein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-186/Product: interferon beta-2 #status predicted <MAT>
F:52-161/Disulfide bonds: #status predicted
F:131,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.2%; Score 482.5; DB 1; Length 186;
Best Local Similarity 56.7%; Pred. No. 3.4e-32;
Matches 93; Conservative 30; Mismatches 40; Indels 1; Gaps 1;

Qy 2 SYNLLGFLQSSNFQCKLLWQLNGRLVCLKDRMNFDPPEIKQLQNFKEDAAALTYI 61
Db 23 SYSLRFFQRRSLALCQKLLRQLPSTPQCLEARMDQFQPEMKQAQFQKEDAILVIYE 82
Qy 62 MLQNIFAIPRODSSSTGWNETHVENLLANVYHQINHLKTVLEKLEKEDFTRGKLMSSL 121
Db 83 MLQIFNILTRDFSSTGWNETHVENLLANVYHQINHLKTVLEKLEKEDFTRGKLMSSL 141
Qy 122 LKRYGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 165
Db 142 LRKYFENLVQLKSKYENRCANTVVRVQLLRNFSEFLRGLTYLR 185

RESULT 3
IVHOB1
Interferon beta-1 precursor - horse
N:Alternate names: EGFN-beta-1; type I interferon
C:Species: Equus caballus (domestic horse)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 22-Jun-1999
C:Accession: G24912
R:Hummel, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.
DNA 5, 345-356, 1986
A:Title: Molecular cloning and expression in Escherichia coli of equine type I interf
A:Reference number: A90956; MUID:87053170
A:Accession: G24912
A:Molecule type: mRNA
A:Residues: 1-186 <HIM>
A:Cross-references: GB:M14546; NID:g164228; PIDN:AAA30954.1; PID:g164229
C:Superfamily: interferon alpha
C:Keywords: antiviral; glycoprotein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-186/Product: interferon beta-1 #status predicted <MAT>
F:101,136/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 54.6%; Score 477.5; DB 1; Length 186;
Best Local Similarity 57.8%; Pred. No. 8.7e-32;
Matches 96; Conservative 27; Mismatches 42; Indels 1; Gaps 1;

Qy 1 MSYNLLGFLQSSNFQCKLLWQLNGRLVCLKDRMNFDPPEIKQLQNFKEDAAALTYI 60
Db 22 VNYDLRSLQSSNSACLMLLRQLNGAPQPCPDPTMNFQVPEIEQAQFQKEDAAALTYI 81
Qy 61 EMLQNIFAIPRODSSSTGWNETHVENLLANVYHQINHLKTVLEKLEKEDFTRGKLMSSL 120
Db 82 EMLQHTWIRFRNFASSTGWNETHVENLLANVYHQINHLKTVLEKLEKEDFTRGKLMSSL 140
Qy 121 HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
Db 141 RLKYYIGRISQYLKAKYSHCAWTIVRVEILRNFFYNRLTGYLRN 186

RESULT 4
IVBOB3
Interferon beta-3 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 07-Feb-1997
C:Accession: A01841
R:Leung, D.W.; Capon, D.J.; Goeddel, D.V.
Bio/Technology 2, 458-464, 1984
A:Title: The structure and bacterial expression of three distinct bovine interferon-b
A:Reference number: A90097


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A;Accession: A01841
A:Molecule type: DNA
A:Residues: 1-186 <LEU>
C:Superfamily: Interferon alpha
C:Keywords: glycoprotein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-186/Product: interferon beta-3 #status predicted <MAT>
F:52-161/Disulfide bonds: #status predicted
F:131,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          51.7%; Score 451.5; DB 1; Length 186;
Best Local Similarity 52.7%; Pred. No. 1.1e-29;
Matches      87; Conservative    34; Mismatches   43; Indels     1; Gaps     1;

QY      2 SYNLGLQRSSNFQCOKLLWQLNGRLEYCLKDRMNFDPPEIKQLQNFskEDAALTYIE 61
        ||| || | || | || | || | :|| :|| :|| :|| :|| :|| :|| :|| :||
DB      23 SYSLLRFQRRSAEVCOKLLCOLHSTQHCEAKMDQVPEEMQAQFRKEDAILVIYE 82
        ||| || | || | || | || | || | :|| :|| :|| :|| :|| :|| :|| :||

QY      62 MLQNIFAIFRDSSSTGWNETIVENLLANYHQINHLKTVLVEEKLEKDEDFTRGKLMSLH 121
        ||| || | || | || | || | || | || | :|| :|| :|| :|| :|| :|| :|| :||
DB      83 MLQIIFNILTRDFSSTGWSGTSEIEDLLVELYGQNNRLPQIQKEIMQEQNTMGD-TIVLH 141

QY      122 LKRYGRILHYLKAKESHCQAWTVRVVEILRNFFYNRLTGYLRN 166
        ||| || | || | || | || | || | || | || | :|| :|| :|| :|| :|| :|| :||
DB      142 LKRYFYFLNVQYLESKEYNRCAWTVVVRVQILTNSFSLMRLTASLRD 186

RESULT      5
IVBOBI
Interferon beta-1 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 07-Feb-1997
C:Accession: A01842
R:Leung, D.W.; Capon, D.J.; Goeddel, D.V.
BioTechnology 2, 458-464, 1984
A:Title: The structure and bacterial expression of three distinct bovine Interf
A:Reference number: A90097
A:Accession: A01842
A:Molecule type: DNA
A:Residues: 1-186 <LEU>
C:Superfamily: Interferon alpha
C:Keywords: glycoprotein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-186/Product: interferon beta-1 #status predicted <MAT>
F:52-161/Disulfide bonds: #status predicted
F:131,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          49.3%; Score 430.5; DB 1; Length 186;
Best Local Similarity 50.3%; Pred. No. 5.7e-28;
Matches      83; Conservative    36; Mismatches   45; Indels     1; Gaps     1;

QY      2 SYNLGLQRSSNFQCOKLLWQLNGRLEYCLKDRMNFDPPEIKQLQNFskEDAALTYIE 61
        ||| || | || | || | || | :|| :|| :|| :|| :|| :|| :|| :||
DB      23 SYSLLRFQQRSLKCECKLLGQLPSTSQHCLEARMDQMPPEMKQEQQFKEDAILVMYE 82
        ||| || | || | || | || | || | :|| :|| :|| :|| :|| :|| :|| :||

QY      62 MLQNIFAIFRDSSSTGWNETIVENLLANYHQINHLKTVLVEEKLEKDEDFTRGKLMSLH 121
        ||| || | || | || | || | || | || | :|| :|| :|| :|| :|| :|| :|| :||
DB      83 VLQHFILTRDFSSTGWSGTSEIEDLLKELKYWMNRLPQIQKEIMQKONSTEDTIVP-H 141

QY      122 LKRYGRILHYLKAKESHCQAWTVRVVEILRNFFYNRLTGYLRN 166
        ||| || | || | || | || | || | || | || | :|| :|| :|| :|| :|| :|| :||
DB      142 LGKYYFLNMVQYLESKEYDRCAWTVVVRVQILTNSFSLMRLTGYVRD 186

RESULT      6
IVMSB
Interferon beta precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 22-Jun-1999
C:Accession: S02020; S04201; A01839
R:Vojdani, G.; Coulombel, C.; Doly, J.
```

J. Mol. Biol. 204, 221-231, 1988

A:Title: Structure and characterization of a murine chromosomal fragment containing

A:Reference number: S02020; MUID:89125582

A:Accession: S02020

A:Molecule type: DNA

A:Residues: 1-182 <VOD>

A:Cross-references: EMBL:X14029; NID:g51550; PIDN:CAA32190.1; PID:g51551

R:Kuga, T.; Fujita, T.; Taniguchi, T.

Nucleic Acids Res. 17, 3291, 1989

A:Title: Nucleotide sequence of the mouse interferon-beta gene.

A:Reference number: S04201; MUID:89263735

A:Accession: S04201

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-182 <UG>

A:Cross-references: EMBL:X14455; NID:g51538; PIDN:CAA32625.1; PID:g51539

R:Higashi, Y.; Sokawa, Y.; Watanabe, Y.; Kawade, Y.; Ohno, S.; Takooka, C.; Taniguchi

J. Biol. Chem. 258, 9522-9529, 1983

A:Title: Structure and expression of a cloned cDNA for mouse interferon-beta.

A:Reference number: A01839; MUID:83265757

A:Accession: A01839

A:Molecule type: mRNA

A:Residues: 1-182 <HIG>

A:Cross-references: GB:X00020; NID:g194113; PIDN:AAA37891.1; PID:g309327

C:Genetics:

C:Map position: 4

C:Superfamily: interferon alpha

C:Keywords: glycoprotein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-182/Product: interferon beta #status predicted <MAT>

F:50,90,97/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.58; Score 336.5; DB 1; Length 182;

Best Local Similarity 45.88; Pred. No. 2.4e-20;

Matches 76; Conservative 26; Mismatches 59; Indels 5; Gaps 3;

Qy 1 MSYLLGFLQSRNFQCKQLWQLNGRLEYCLKQRMNFDPDEETIKQLQKPSKEDAAALTY 60

Db 22 INYKQLQERTNTRKCOELLEQLNGKIN--LTTRADEFKIPDEM--TEKMOKSYTAFIQ 77

Qy 61 EMLQNIFAIFRODSSSTGWNETIVENLANYHYQHILKTVLEBKLEKEDFTRGKLMSSL 120

Db 78 EMLQNVFLVRNFSSTGWNETIVRLLDELHQQTFLVKTVLEBK--QERLTWEMSSAL 136

Qy 121 HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFFNRLTGYLRLN 166

Db 137 HLKSYRWQRYLKLKMYNSAMWVRAEIPRNFELIIRLRTNRFQN 182

RESULT 7

JC5424

interferon beta precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000

C:Accession: JC5424

R:Yokoyama, S.; Ohishi, N.; Shamoto, M.; Watanabe, Y.; Yagi, K.

Biochem. Biophys. Res. Commun. 232, 698-701, 1997

A:Title: Isolation and expression of rat interferon beta gene and growth-inhibitory

A:Reference number: JC5424; MUID:97271387

A:Accession: JC5424

A:Molecule type: DNA

A:Residues: 1-184 <YOK>

A:Cross-references: DDBJ:DB7919; NID:g1616938; PIDN:BAAL3502.1; PID:g1616939

C:Comment: This protein exhibits characteristic antiviral and antitumor activities.

C:Genetics:

A:Gene: IFNBeta

C:Superfamily: interferon alpha

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-184/Product: interferon beta #status predicted <MAT>

Query Match 37.68; Score 328.5; DB 2; Length 184;

Query Match 29.4%; Score 257; DB 1; Length 184;
Best Local Similarity 36.0%; Pred. No. 6.7e-14;
Matches 54; Conservative 28; Mismatches 54; Indels 14; Gaps 1;

125 YYGRILHYLKAKEYSHCAWTIVRVEILRNF 154
| : | | : | : | | | | | : | : |
146 YFORIALYLOEKYSPCAMEIVRAETMRSE 175

Residues: 1-184 <HIM>
Cross-references: GB:M14540; NID:gl164226; PIDN:AAA30953.1; PID:gl164227
Keywords: interferon alpha
Superfamily: interferon alpha
Keywords: antiviral
1-1-23/domain: signal sequence #status predicted <SIG>
1-24-184/Prodomain: interferon alpha-1 #status predicted <MAT>
24-124-152-162/Disulfide bonds: #status predicted

5 LGFGFGRSSNFCQCKLLWQLNGRLLEYCLKORMFNFDPEETIKQLONPSKEDAALTYEMIQ 64
y y
d d
40 LUGQMRRISPS-----CLKORNFDFGPFVDGNQFKPOALSVAHETIQ 85
y y
d d
65 NTAIFRODSSSTGWNETIVENLANYHOINHLKTVLEKLEKEKEDFTRGKLMSDLHKR 124
y y
d d
86 QIHFLEFDGSAMDESLLDKLTGLYQOLTLEACLSEQGVVEETPLMNEDSLLAVRR 145
y y
125 YYGRILHYLKAREYSHCAWTIVRVIELRNFF 154
y y
146 YEORALYLOEKKYSPCAWEIVRAEIMRSF 175
y y

Species: Equus caballus (domestic horse)
Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Jun-1999

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2002, 15:44:50 ; Search time 46.62 Seconds
(without alignments)
615.984 Million cell updates/sec

Title: SEQ2-49N-51T
Perfect score: 875
Sequence: 1 MSYNLGLFLQRSSNFOCQKL.....RVEILRNFYFINRLTYGLRN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_19:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Length | DB | ID | Description |
|------------|-------|-------|--------|----|--------|--------------------|
| 1 | 821 | 93.8 | 187 | 6 | 077812 | 077812 macaca fasc |
| 2 | 816 | 93.3 | 187 | 4 | Q15943 | Q15943 homo sapien |
| 3 | 524.5 | 59.9 | 186 | 6 | Q29412 | Q29412 sus scrofa |
| 4 | 254.5 | 29.1 | 195 | 6 | Q9GLL5 | Q9GLL5 bos taurus |
| 5 | 249.5 | 28.5 | 189 | 4 | Q14618 | Q14618 homo sapien |
| 6 | 244.5 | 27.9 | 188 | 4 | Q96K16 | Q96K16 homo sapien |
| 7 | 244 | 27.9 | 195 | 6 | Q28844 | Q28844 oryctolagus |
| 8 | 243 | 27.8 | 189 | 6 | Q95J78 | Q95J78 saguinus oe |
| 9 | 241 | 27.5 | 189 | 6 | Q95J77 | Q95J77 saguinus oe |
| 10 | 240.5 | 27.3 | 189 | 4 | Q14607 | Q14607 homo sapien |
| 11 | 238.5 | 27.3 | 195 | 6 | Q9GLL6 | Q9GLL6 bos taurus |
| 12 | 236 | 27.0 | 174 | 4 | Q13168 | Q13168 homo sapien |
| 13 | 236 | 27.0 | 195 | 6 | Q28845 | Q28845 oryctolagus |
| 14 | 236 | 27.0 | 195 | 6 | Q28562 | Q28562 ovis aries |
| 15 | 236 | 27.0 | 195 | 6 | Q28545 | Q28545 ovis aries |
| 16 | 235.5 | 26.9 | 189 | 4 | Q14639 | Q14639 homo sapien |

| | | | | | | |
|----|-------|------|-----|----|--------|--------------------|
| 17 | 235.5 | 26.9 | 195 | 6 | Q9MYK6 | Q9MYK6 bos taurus |
| 18 | 235.5 | 26.9 | 195 | 6 | Q95NE2 | Q95NE2 bos taurus |
| 19 | 234 | 26.7 | 195 | 6 | Q28843 | Q28843 oryctolagus |
| 20 | 234 | 26.7 | 195 | 6 | Q28847 | Q28847 oryctolagus |
| 21 | 234 | 26.7 | 195 | 6 | Q28561 | Q28561 ovis aries |
| 22 | 225 | 25.7 | 190 | 6 | Q29085 | Q29085 sus scrofa |
| 23 | 224.5 | 25.7 | 179 | 6 | Q29084 | Q29084 sus scrofa |
| 24 | 222.5 | 25.4 | 195 | 6 | P28170 | P28170 ovis aries |
| 25 | 220.5 | 25.2 | 181 | 4 | Q14608 | Q14608 homo sapien |
| 26 | 219 | 25.0 | 190 | 6 | Q29098 | Q29098 sus scrofa |
| 27 | 218 | 24.9 | 190 | 11 | Q9ES91 | Q9ES91 marmota mon |
| 28 | 217 | 24.8 | 166 | 4 | Q9UMJ3 | Q9UMJ3 homo sapien |
| 29 | 217 | 24.8 | 189 | 4 | Q14605 | Q14605 homo sapien |
| 30 | 215.5 | 24.6 | 207 | 4 | Q9P0W0 | Q9P0W0 homo sapien |
| 31 | 212 | 24.2 | 190 | 11 | Q61719 | Q61719 mus musculu |
| 32 | 208 | 23.8 | 190 | 11 | Q99N22 | Q99N22 marmota mon |
| 33 | 200 | 22.9 | 190 | 11 | Q64138 | Q64138 cricetinae |
| 34 | 197 | 22.5 | 84 | 6 | Q95LB8 | Q95LB8 sus scrofa |
| 35 | 195.5 | 22.3 | 170 | 6 | Q29114 | Q29114 sus scrofa |
| 36 | 193.5 | 22.1 | 170 | 6 | Q29115 | Q29115 sus scrofa |
| 37 | 193 | 22.1 | 190 | 11 | Q61718 | Q61718 mus musculu |
| 38 | 193 | 22.1 | 190 | 11 | Q91WX3 | Q91WX3 sigmodon hi |
| 39 | 188 | 21.5 | 108 | 6 | Q9N1U6 | Q9N1U6 equus cabal |
| 40 | 186 | 21.3 | 166 | 6 | P79228 | P79228 odocoileus |
| 41 | 185 | 21.1 | 190 | 11 | Q61716 | Q61716 mus musculu |
| 42 | 180 | 20.6 | 136 | 11 | Q61717 | Q61717 mus musculu |
| 43 | 150.5 | 17.2 | 182 | 11 | Q9R1T0 | Q9R1T0 mus musculu |
| 44 | 147.5 | 16.9 | 193 | 13 | Q9PW15 | Q9PW15 gallus gall |
| 45 | 132.5 | 15.1 | 193 | 13 | Q9PW16 | Q9PW16 gallus gall |

ALIGNMENTS

| | |
|--------|---|
| RESULT | 1 |
| 077812 | |
| ID | 077812 PRELIMINARY; PRT; 187 AA. |
| AC | 077812; |
| DT | 01-NOV-1998 (Tremblrel. 08, Created) |
| DT | 01-NOV-1998 (Tremblrel. 08, Last sequence update) |
| DT | 01-DEC-2001 (Tremblrel. 19, Last annotation update) |
| DE | INTERFERON BETA. |
| GN | IFN-BETA. |
| OS | Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; |
| OC | Cercopitheciinae; Macaca. |
| OX | NCBI_TaxID=9541; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RX | MEDLINE=99156140; PubMed=10048395; |
| RA | Mathew F., Le Grand R., Rousseau V., De Maeyer E., Dormont D., |
| RA | Lauret E.; |
| RT | "Macaque lymphocytes transduced by a constitutively expressed |
| RT | interferon beta gene display an enhanced resistance to SIMmac251 |
| RT | infection." |
| RL | Hum. Gene Ther. 10:429-429(1999). |
| CC | - SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA |
| CC | FAMILY. |
| CC | EMBL; AJ011909; CAA09862.1; -. |
| DR | HSSP; P01574; IAU1. |
| DR | InterPro; IPR000471; Interferon_abd. |
| DR | Pfam; PF00143; Interferon; 1. |
| DR | PRINTS; PR00266; INTERFERONAB. |
| DR | PRODOM; PD000550; Interferon_abd; 1. |
| DR | SMART; SM00076; IFabd; 1. |
| DR | PROSITE; PS00252; INTERFERON_A_B_D; 1. |
| KW | Antiviral; Cytokine. |
| SQ | SEQUENCE 187 AA; 22266 MW; 376AEF7332B7807 CRC64; |

Query Match 93.8%; Score 821; DB 6; Length 187;
Best Local Similarity 92.8%; Pred. No. 1e-63;

```

Matches 154; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
QY 1 MSYNLLGFLQSSNFQCKLLWLNGLRLEYCLKDRMNFDPPEETKQlQnFKEDAALTYI 60
D 22 MSYNLLGFLQSSNFQCKLLWLNGLRLEYCLKDRMNFDPPEETKQlQnFKEDAALTYI 81
QY 61 EMLQNIFAIFRQDSSSTGWNTEIVENLLANYHQLNHLKTVLEKLEKEDFTGRKLMSSL 120
D 82 EMLQNIFAIFRQDSSSTGWNTEIVENLLANYHQLNHLKTVLEKLEKEDFTGRKLMSSL 141
QY 121 HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
D 142 HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 187

RESULT 2
Q15943
ID Q15943 PRELIMINARY; PRT; 187 AA.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERFERON-BETA-1 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065590; PubMed=6183692;
RA Fiers W., Remaut E., Devos R., Cheroutre H., Contreras R.R.,
RA Gheysen D., Degraeve W.M., Stanssens P., Tavernier J., Taya I.,
RA Content J.;
RT "The human fibroblast and human immune interferon genes and their
RT expression in homologous and heterologous cells.";
RL Philos. Trans. R. Soc. Lond., B, Biol. Sci. 299:29-38(1982).
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
DR EMBL; M25460; AAC41702.1; -.
DR HSSP; P01574; 1AU1.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; Ifabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; UNKNOWN_1.
KW Antiviral; Cytokine; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 187 INTERFERON-BETA.
FT SEQUENCE 187 AA; 22251 MW; D8E65B694862061 CRC64;

Query Match 93.3%; Score 816; DB 4; Length 187;
Best Local Similarity 94.6%; Pred. No. 2.8e-63;
Matches 157; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 1 MSYNLLGFLQSSNFQCKLLWLNGLRLEYCLKDRMNFDPPEETKQlQnFKEDAALTYI 60
D 22 MSYNLLGFLQSSNFQCKLLWLNGLRLEYCLKDRMNFDPPEETKQlQnFKEDAALTYI 81
QY 61 EMLQNIFAIFRQDSSSTGWNTEIVENLLANYHQLNHLKTVLEKLEKEDFTGRKLMSSL 120
D 82 EMLQNIFAIFRQDSSSTGWNTEIVENLLANYHQLNHLKTVLEKLEKEDFTGRKLMSSL 141
QY 121 HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
D 142 HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 187

RESULT 3
Q29412
ID Q29412 PRELIMINARY; PRT; 186 AA.
AC Q29412;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERFERON-BETA-1 PRECURSOR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Artursson K., Gobl A., Lindersson M., Johansson M., Alm G.;
RA Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92348930; PubMed=1640116;
RA Artursson K., Gobl A., Lindersson M., Johansson M., Alm G.;
RA "Molecular cloning of a gene encoding porcine interferon-beta.";
RL J. Interferon Res. 12:153-160(1992).
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
DR EMBL; M86762; AAA31056.1; -.
DR EMBL; S41178; AAB22723.1; -.
DR HSSP; P01574; 1AU1.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; Ifabd; 1.
KW Antiviral; Cytokine; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 186 INTERFERON-BETA-1.
FT SEQUENCE 186 AA; 21878 MW; 5F16B8B3C3AE603D CRC64;

Query Match 59.9%; Score 524.5; DB 6; Length 186;
Best Local Similarity 60.8%; Pred. No. 5e-38;
Matches 101; Conservative 28; Mismatches 36; Indels 1; Gaps 1;
QY 1 MSYNLLGFLQSSNFQCKLLWLNGLRLEYCLKDRMNFDPPEETKQlQnFKEDAALTYI 60
D 22 MSYNLLGFLQSSNFQCKLLWLNGLRLEYCLKDRMNFDPPEETKQlQnFKEDAALTYI 81
QY 61 EMLQNIFAIFRQDSSSTGWNTEIVENLLANYHQLNHLKTVLEKLEKEDFTGRKLMSSL 120
D 82 EMLQNIFAIFRQDSSSTGWNTEIVENLLANYHQLNHLKTVLEKLEKEDFTGRKLMSSL 140
QY 121 HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
D 141 HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 186

RESULT 4
Q9GLL5
ID Q9GLL5 PRELIMINARY; PRT; 195 AA.
AC Q9GLL5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERFERON TAU.
GN IFN-TAU-C1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Chung Y.G., Seidel G.E. Jr.;
RA "Cloning bovine interferon-tau genes and characterizing their
RA transcriptional expression during early pregnancy.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.

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[illegible]


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Query Match      27.5%; Score 240.5; DB 4; Length 189;
Best Local Similarity 37.4%; Pred. No. 2.le-13;
Matches 58; Conservative 22; Mismatches 58; Indels 17; Gaps 4;

Qy 20 LLWQLNGRL--YCLKDRMNDIPEIKQLQFTKEDAAALTIYEMQLQNFQAFIRQDSSST 77
Db 40 LLAQN-GRISPPSCUKDRHFRPEEFDFGHQFQKTAISVLHHEMIQOQFNLFSTEDSSA 98
Qy 78 GWNQETIVENLLANYHQINHLKT-----VLEEKLEKEDFTRGKLMSSHLKRYGYRIL 130
Db 99 AWEQSLEKSTELQQLNDLEACVYQEVGVSETPLMNEFDI-----LAVRKYQRIT 151
Qy 131 HYLKAKKEYSHCAWTIVRVEILRNFYFINRLTGYLR 165
Db 152 LYLTEKYSPCAWEVVRAEIMRSFSFSTNLKKGLR 186

RESULT 11
Q9GLL6 PRELIMINARY; PRT; 195 AA.
AC Q9GLL6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERFERON TAU.
GN IFN-TAU-C3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN SEQUENCE FROM N.A.
RA Chung Y.G., Seidel G.E. Jr.;
RT "Cloning bovine interferon-tau genes and characterizing their
RT transcriptional expression during early pregnancy.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
DR EMBL; AF238611; AAG14168.1; -.
DR HSSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR Antiviral; Cytokine.
KW Bos taurus (Bovine).
FT NON_TER 1
SQ SEQUENCE 195 AA; 22160 MW; 6DB1FAE39BF033FA CRC64;

Query Match      27.3%; Score 238.5; DB 6; Length 195;
Best Local Similarity 37.5%; Pred. No. 3.2e-13;
Matches 51; Conservative 29; Mismatches 53; Indels 3; Gaps 2;

Qy 19 KLLWQLNGRL--EYCLKDRMNDIPEIKQLQFTKEDAAALTIYEMQLQNFQAFIRQDSSS 76
Db 39 RLLARMN-RLSPHCLQDRKDFGLPQEWEGSQQLQKQAISVLHHEMIQOQFNLFHIEHSS 97
Qy 77 TGWNQETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSHLKRYGYRILHYIKAK 136
Db 98 AAWNTTLEQLCTGLQQLQLEDLQACGLPVGMEKSDMRGMPILTIVKKYFHDHVLKKE 157
Qy 137 EYSHCAWTIVRVEILR 152
Db 158 EYSDCAWEIIRVEMMR 173

RESULT 12
Q13168 PRELIMINARY; PRT; 174 AA.
ID Q13168
AC Q13168;
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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERFERON OMEGA-1 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RA Zeng Q., Li M., Zhou Y., Guo H., Hou Y.;
RT "The cloning, sequencing of the primary structure and expression in E.
RT coli Chinese human IFN-W1 gene.";
RL Sci. China B. 0:0-0(0).
RN [2]
RN SEQUENCE FROM N.A.
RA Xu L.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
DR EMBL; U25670; AAA70091.1; -.
DR HSSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
DR Antiviral; Cytokine.
KW NON_TER 1
FT NON_TER 1
SQ SEQUENCE 174 AA; 20249 MW; BICC9AB5993016C5 CRC64;

Query Match      27.0%; Score 236; DB 4; Length 174;
Best Local Similarity 33.8%; Pred. No. 4.6e-13;
Matches 46; Conservative 32; Mismatches 58; Indels 0; Gaps 0;

Qy 31 CLKDRMNFDPPEIKQLQNFQAFIRQDSSSTGWNQETIVENLLAN 90
Db 31 CLKDRMNFDPPEIKQLQNFQAFIRQDSSSTGWNQETIVENLLAN 90
Qy 91 VYHQINHLKTVLEEKLEKEDFTRGKLMSSHLKRYGYRILHYIKAKYSHCAWTIVRVEI 150
Db 91 LHQQLHLETCLLQVGVGESAGAISSPALTLLRRYFQIRVYLKKEKYSDCAWEDRMEI 150
Qy 151 LRNEYFINRLTGYLRN 166
Db 151 MKSLFLSTNMQERLRS 166

RESULT 13
Q28845 PRELIMINARY; PRT; 195 AA.
AC Q28845;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERFERON-OMEGA45.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RN SEQUENCE FROM N.A.
RA MEDLINE=94132653; PubMed=8301151;
RA Charlier M., L'Haridon R., Bolsnard M., Martal J., Gave P.;
RT "Cloning and structural analysis of four genes encoding interferon-
RT omega in rabbit.";
RL J. Interferon Res. 13:313-322(1993).
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
DR EMBL; S69000; AAC60526.1; -.
DR HSSP; P01563; 2HIE.
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DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
SQ SEQUENCE 195 AA; 21996 MW; 395EE700C586A928 CRC64;

Query Match 27.0%; Score 236; DB 6; Length 195;
Best Local Similarity 39.5%; Pred. No. 5.3e-13;
Matches 49; Conservative 20; Mismatches 55; Indels 0; Gaps 0;

QY 31 CLKDRMFDIPEEIKQLQNFKEADAALTIYEMLQNIFAIFRQDSSSTGWNETIVENLLAN 90
Db 52 CLKDRRDFQFPREVNGSQFQKNQTVSVLHMLQIFNLLHTARSSAANNNTLLEELHTA 111

QY 91 VYHGINHLKTVLEKLEKEDFTRGKLMSSHLKRYGRILHYLKAKEYSHCAWTIVRVEI 150
Db 112 LHQQLQGLTCLVQAMGEEDSVLTADSPITMLKRYFQIRLYLDEKKHSGCAWELVRMEI 171

QY 151 LRNF 154
Db 172 RRAF 175

RESULT 14
Q28562 PRELIMINARY; PRT; 195 AA.
ID Q28562
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ovine INTERFERON ALPHA PRECURSOR.
GN AMY 49.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=92039090; PubMed=1937057;
RA Whaley A.E., Carroll R.S., Inakawa K.;
RT "Cloning and analysis of a gene encoding ovine interferon alpha-II.";
RL Gene 106:281-282(1991).
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.
CC EMBL; X59068; CAA41791.1; -.
DR HSSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 195 OVINE INTERFERON ALPHA.
FT SEQUENCE 195 AA; 22006 MW; 3B8EE700C586A928 CRC64;

Query Match 27.0%; Score 236; DB 6; Length 195;
Best Local Similarity 39.5%; Pred. No. 5.3e-13;
Matches 49; Conservative 20; Mismatches 55; Indels 0; Gaps 0;

QY 31 CLKDRMFDIPEEIKQLQNFKEADAALTIYEMLQNIFAIFRQDSSSTGWNETIVENLLAN 90
Db 52 CLKDRRDFQFPREVNGSQFQKNQTVSVLHMLQIFNLLHTARSSAANNNTLLEELHTA 111

QY 91 VYHGINHLKTVLEKLEKEDFTRGKLMSSHLKRYGRILHYLKAKEYSHCAWTIVRVEI 150

Db 112 LHQQLQGLTCLVQAMGEEDSVLTADSPITMLKRYFQIRLYLDEKKHSGCAWELVRMEI 171
QY 151 LRNF 154
Db 172 RRAF 175

RESULT 15
Q28545 PRELIMINARY; PRT; 195 AA.
ID Q28545
AC Q28545;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERFERON TYPE I PRECURSOR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96219886; PubMed=8639714;
RA Liu L., Leaman D.W., Bixby J.A., Roberts R.M.;
RT "A type I ovine interferon with limited similarity to IFN-alpha, IFN-omega and IFN-tau: gene structure, biological properties and unusual species specificity.";
RL Biochim. Biophys. Acta, Gene Struct. Expr. 1294:55-62(1996).
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.
CC EMBL; U26254; AAB06828.1; -.
DR HSSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 195 INTERFERON TYPE I.
FT SEQUENCE 195 AA; 22010 MW; 15C4CD45D582F86E CRC64;

Query Match 27.0%; Score 236; DB 6; Length 195;
Best Local Similarity 39.5%; Pred. No. 5.3e-13;
Matches 49; Conservative 20; Mismatches 55; Indels 0; Gaps 0;

QY 31 CLKDRMFDIPEEIKQLQNFKEADAALTIYEMLQNIFAIFRQDSSSTGWNETIVENLLAN 90
Db 52 CLKDRRDFQFPREVNGSQFQKNQTVSVLHMLQIFNLLHTARSSAANNNTLLEELHTA 111

QY 91 VYHGINHLKTVLEKLEKEDFTRGKLMSSHLKRYGRILHYLKAKEYSHCAWTIVRVEI 150
Db 112 LHQQLQGLTCLVQAMGEEDSVLTADSPITMLKRYFQIRLYLDEKKHSGCAWELVRMEI 171

QY 151 LRNF 154
Db 172 RRAF 175

Search completed: July 29, 2002, 15:44:50
Job time: 196 sec

| Result No. | Query | | | DB | ID | Description |
|------------|-------|-------|--------|----|------------|--------------------|
| | Score | Match | Length | | | |
| 1 | 864 | 59.9 | 187 | 1 | INB_HUMAN | P01574 homo sapien |
| 2 | 516.5 | 59.1 | 186 | 1 | INB_FELCA | Q9A2J0 felis silve |
| 3 | 482.5 | 55.2 | 186 | 1 | INB2_BOVIN | P01576 bos taurus |
| 4 | 477.5 | 54.6 | 186 | 1 | INB_HORSE | P05012 equus cabal |
| 5 | 451.5 | 51.7 | 186 | 1 | INB3_BOVIN | P01577 bos taurus |
| 6 | 430.5 | 49.3 | 186 | 1 | INB1_BOVIN | P01578 bos taurus |
| 7 | 336.5 | 38.5 | 182 | 1 | INB_MOUSE | P01575 mus musculu |
| 8 | 328.5 | 37.6 | 184 | 1 | INB_RAT | P70499 rattus norv |
| 9 | 284 | 32.5 | 195 | 1 | INB2_HORSE | P05002 equus cabal |
| 10 | 283 | 30.1 | 195 | 1 | INB1_HORSE | P05001 equus cabal |
| 11 | 257 | 29.4 | 184 | 1 | INB1_HORSE | P05003 equus cabal |
| 12 | 257 | 29.4 | 184 | 1 | INB3_HORSE | P05005 equus cabal |
| 13 | 257 | 29.4 | 184 | 1 | INB4_HORSE | P05006 equus cabal |
| 14 | 255.5 | 29.2 | 195 | 1 | INT_CREEL | Q46633 cervus elap |
| 15 | 253 | 28.9 | 184 | 1 | INB2_HORSE | P05004 equus cabal |
| 16 | 250.5 | 28.7 | 189 | 1 | INAF_HUMAN | P05015 homo sapien |
| 17 | 247.5 | 28.3 | 195 | 1 | INB1_BOVIN | P07352 bos taurus |
| 18 | 246.5 | 28.2 | 172 | 1 | INT2_BOVIN | P56830 bos taurus |
| 19 | 245.5 | 28.1 | 195 | 1 | INT6_SHEEP | Q29429 ovis aries |
| 20 | 244.5 | 28.0 | 188 | 1 | INB2_HUMAN | P01563 homo sapien |
| 21 | 244 | 27.9 | 195 | 1 | INB1_HUMAN | P05000 homo sapien |
| 22 | 243.5 | 27.9 | 189 | 1 | INB4_HUMAN | P05014 homo sapien |
| 23 | 243.5 | 27.9 | 195 | 1 | INT1_SHEEP | P56828 ovis aries |
| 24 | 243.5 | 27.9 | 195 | 1 | INT2_SHEEP | P56829 ovis aries |
| 25 | 241.5 | 27.6 | 189 | 1 | INB5_HUMAN | P01569 homo sapien |
| 26 | 241.5 | 27.6 | 189 | 1 | INB7_HUMAN | P01567 homo sapien |
| 27 | 240.5 | 27.5 | 195 | 1 | INT5_SHEEP | Q28595 ovis aries |
| 28 | 239.5 | 27.4 | 172 | 1 | INT3_BOVIN | P56831 bos taurus |
| 29 | 239.5 | 27.4 | 195 | 1 | INT1_BOVIN | P15696 bos taurus |
| 30 | 239.5 | 27.4 | 195 | 1 | INT7_SHEEP | Q08071 ovis aries |
| 31 | 239.5 | 27.4 | 195 | 1 | INTB_SHEEP | Q28169 ovis aries |
| 32 | 238.5 | 27.3 | 189 | 1 | INB3_HUMAN | P01571 homo sapien |
| 33 | 238.5 | 27.3 | 195 | 1 | INT4_SHEEP | Q28594 ovis aries |


```
Db 22 VNYDLRSQSRSSNACLMLLRLQLNGAPQRCPTDMNFQVPEIEQAQOFQKEDAAIYI 81
QY 61 EMLQNIFAIPRODSSSTGWNTEIVENLVYHQLNHLKTVLEEKLEKEDFTGRKLMSSL 120
Db 82 EMLQHTWRIFRNFASSTGWNTEIVENLVYHQLNHLKTVLEEKLEKEDFTGRKLMSSL 140
QY 121 HKRYGYRILHYLKAKEYSHCAWTIVRVYILRNFEYFINRLTGYLRN 166
Db 141 LKYYGRISOLYLRKAKYSHCAWTIVRVYILRNFEYFINRLTGYLRN 186

RESULT 5
INB3_BOVIN STANDARD; PRT; 186 AA.
AC P01577;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Interferon beta-3 precursor.
GN IFNB3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Leung D.W., Capon D.J., Goeddel D.V.;
RT "The structure and bacterial expression of three distinct bovine
RT interferon-beta genes.";
RL Biotechnology 2:458-464(1984).
CC -!- FUNCTION: HAS ANTIVIRAL, ANTIBACTERIAL AND ANTICANCER ACTIVITIES.
CC -!- SUBUNIT: MONOMER.
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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CC -----
CC EMBL; M15479; AAA30581.1; -.
CC PIR; A01841; IVBOB3.
CC HSSP; P01574; 1AUI.
CC InterPro; IPR000471; Interferon_abd.
CC Pfam; PF00143; Interferon; 1.
CC PRINTS; PR00266; INTERFERONAB.
CC ProDom; PD000550; Interferon_abd; 1.
CC SMART; SM00076; IFabd; 1.
CC PROSITE; PS00252; INTERFERON_A_B_D; 1.
CC Cytokine; Glycoprotein; Antiviral; Multigene family; Signal.
CC SIGNAL 1 21
CC CHAIN 22 186 INTERFERON BETA-3.
CC DISULFID 52 161 PROBABLE.
CC CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 186 AA; 22059 MW; 1D1011EBE1A65D CRC64;

Query Match 51.7%; Score 451.5; DB 1; Length 186;
Best Local Similarity 52.7%; Pred. No. 9e-31;
Matches 87; Conservative 34; Mismatches 43; Indels 1; Gaps 1;

QY 2 SYNLLGFLQSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEIKQLQNFsKEDAAIYI 61
Db 23 SYSLRFRQRRSAEVCKLLGQLHSTPHQCLEAKMDFQVPEEMQAQOFKEDAILVYI 82
QY 62 MLQNIFAIPRODSSSTGWNTEIVENLVYHQLNHLKTVLEEKLEKEDFTGRKLMSSL 121
Db 83 MLQOIFNLRDFSTGWNTEIVENLVYHQLNHLKTVLEEKLEKEDFTGRKLMSSL 141
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QY 122 LKRYGYRILHYLKAKEYSHCAWTIVRVYILRNFEYFINRLTGYLRN 166
Db 142 LKYYFNLYVOYLESKEYNRCAWTVVRVQILTNFSFLMRLTASLRD 186

RESULT 6
INB1_BOVIN STANDARD; PRT; 186 AA.
AC P01578;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Interferon beta-1 precursor.
GN IFNB1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Leung D.W., Capon D.J., Goeddel D.V.;
RT "The structure and bacterial expression of three distinct bovine
RT interferon-beta genes.";
RL Biotechnology 2:458-464(1984).
CC -!- FUNCTION: HAS ANTIVIRAL, ANTIBACTERIAL AND ANTICANCER ACTIVITIES.
CC -!- SUBUNIT: MONOMER.
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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CC -----
CC EMBL; M15477; AAA30579.1; -.
CC PIR; A01842; IVBOB1.
CC HSSP; P01574; 1AUI.
CC InterPro; IPR000471; Interferon_abd.
CC Pfam; PF00143; Interferon; 1.
CC PRINTS; PR00266; INTERFERONAB.
CC ProDom; PD000550; Interferon_abd; 1.
CC SMART; SM00076; IFabd; 1.
CC PROSITE; PS00252; INTERFERON_A_B_D; 1.
CC Cytokine; Glycoprotein; Antiviral; Multigene family; Signal.
CC SIGNAL 1 21
CC CHAIN 22 186 INTERFERON BETA-1.
CC DISULFID 52 161 PROBABLE.
CC CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 186 AA; 22195 MW; F9060C07EA415B9C CRC64;

Query Match 49.3%; Score 430.5; DB 1; Length 186;
Best Local Similarity 50.3%; Pred. No. 4.9e-29;
Matches 83; Conservative 36; Mismatches 45; Indels 1; Gaps 1;

QY 2 SYNLLGFLQSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEIKQLQNFsKEDAAIYI 61
Db 23 SYSLRFRQRRSAEVCKLLGQLHSTPHQCLEAKMDFQVPEEMQAQOFKEDAILVYI 82
QY 62 MLQNIFAIPRODSSSTGWNTEIVENLVYHQLNHLKTVLEEKLEKEDFTGRKLMSSL 121
Db 83 VLQIHFGILTRDFSTGWNTEIVENLVYHQLNHLKTVLEEKLEKEDFTGRKLMSSL 141

QY 122 LKRYGYRILHYLKAKEYSHCAWTIVRVYILRNFEYFINRLTGYLRN 166
Db 142 LKYYFNLYVOYLESKEYNRCAWTVVRVQILTNFSFLMRLTGYVRD 186
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RESULT 7
INB_MOUSE
ID INB_MOUSE STANDARD; PRT; 182 AA.
AC P01575;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interferon beta precursor (IFN-beta).
GN IFNB OR IFB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
ON [1]
RX SEQUENCE FROM N.A.
RP MEDLINE=8326575; PubMed=6688252;
RA Higashi Y., Sokawa Y., Watanabe Y., Kawade Y., Ohno S., Takaoka C.,
RA Taniguchi T.;
RT "Structure and expression of a cloned cDNA for mouse interferon-
RT beta.";
RL J. Biol. Chem. 258:9522-9529(1983).
[2]
RX SEQUENCE FROM N.A.
RP MEDLINE=89263735; PubMed=2726460;
RA Kuga T., Fujita T., Taniguchi T.;
RT "Nucleotide sequence of the mouse interferon-beta gene.";
RL Nucleic Acids Res. 17:3291-3291(1989).
[3]
RX SEQUENCE FROM N.A.
RP MEDLINE=8912582; PubMed=3221389;
RA Vojdani G., Coulombel C., Doly J.;
RT "Structure and characterization of a murine chromosomal fragment
RT containing the interferon beta gene.";
RL J. Mol. Biol. 204:221-231(1988).
[4]
RX STRUCTURE OF CARBOHYDRATES
RP MEDLINE=88196115; PubMed=3360010;
RA Clivas A., Fournet B., Coulombel C., le Roscouet D., Honvault A.,
RA Shimizu H., Mizuno H., Mitsui Y.;
RT "Three-dimensional structure of recombinant murine interferon-beta.";
Proc. Jpn. Acad., B, Phys. Biol. Sci. 66:77-80(1990).
[6]
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RP MEDLINE=92371425; PubMed=1505514;
RA Senda T., Shimazu T., Matsuda S., Kawano G., Shimizu H.,
RA Nakamura K.T., Mitsui Y.;
RT "Three-dimensional crystal structure of recombinant murine interferon-
RT beta.";
RL EMBO J. 11:3193-3201(1992).
[7]
RX X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
RP MEDLINE=96028219; PubMed=7473712;
RA Senda T., Saitoh S.-I., Mitsui Y.;
RT "Refined crystal structure of recombinant murine interferon-beta at
RT 2.15-A resolution.";
RL J. Mol. Biol. 253:187-207(1995).
CC -1- FUNCTION: HAS ANTIVIRAL, ANTIBACTERIAL AND ANTICANCER ACTIVITIES.
CC -1- SUBUNIT: MONOMER.
CC -1- PTM: THIS BETA INTERFERON DOES NOT HAVE A DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
-----
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DR EMBL; K00020; AAA37891.1; -
DR EMBL; X14455; CAA32625.1; -
DR EMBL; X14029; CAA32190.1; -
DR PIR; A01839; IVMSB.
DR PIR; S02020; S02020.
DR PDB; 1IFA; 31-JAN-94.
DR PDB; 2HIF; 31-AUG-94.
DR PDB; 1RMI; 14-FEB-95.
DR MGI; 107657; Ifnb.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SK00076; IFabd; 1.
DR PROSITE; PS00232; INTERFERON_A_B_D; 1.
KW Cytokine; Glycoprotein; Antiviral; Signal; 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 182 INTERFERON BETA.
FT CARBOHYD 50 50 N-LINKED (GLCNAC. .).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. .).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. .).
SQ SEQUENCE 182 AA; 8C4C32947FD1B917 CRC64;
Query Match 38.5%; Score 336.5; DB 1; Length 182;
Best Local Similarity 45.8%; Pred. No. 2.9e-21;
Matches 76; Conservative 26; Mismatches 59; Indels 5; Gaps 3;
QY 1 MSYNLLGFLQRSSNFQCKLLWOLNGRLVCYCLKDRMNFDPDEIKQLQDFSKDAALTIY 60
Db 22 INYKQLQERTNIRKQELLEQLNGKIN--LTYRDFKIPNEM--TEKMQKSTAFAIQ 77
QY 61 EMLQNTFAIPQDSSSTGWNETIVENLLANYHQINHLKTVLEKLEKEDFTRGKLMSSL 120
Db 78 EMLQNVFLVFNFSSTGWNETIVVRLDELHQQTVELKTVLEBK-QBERLTWEMSSPAL 136
QY 121 HLKRYGRILHYLKAKKEYSHCAWTIVRVETLRNFYFNRLTGYLRN 166
Db 137 HLKSYWRVQRVQLKLMKYNKYAMVVRVRAEIRNLIIRLTRNFQN 182
RESULT 8
INB_RAT
ID INB_RAT STANDARD; PRT; 184 AA.
AC F70499;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Interferon beta precursor (IFN-beta).
GN Ifnb.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
ON [1]
RX SEQUENCE FROM N.A.
RP STRAIN=Wistar; Tissue=Liver;
RC MEDLINE=97271387; PubMed=9126336;
RA Yokoyama S., Ohishi N., Shamoto M., Watanabe Y., Yagi K.;
RT "Isolation and expression of rat interferon beta gene and growth-
RT inhibitory effect of its expression on rat glioma cells.";
RL Biochem. Biophys. Res. Commun. 232:698-701(1997).
CC -1- FUNCTION: HAS ANTIVIRAL, ANTIBACTERIAL AND ANTICANCER ACTIVITIES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- PTM: THIS BETA INTERFERON DOES NOT HAVE A DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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CC
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CC -----
DR EMBL; D87919; BAA13502.1; -.
DR HSSP; P01575; 2HIF.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Cytokine; Antiviral; Glycoprotein; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 184 INTERFERON BETA.
FT CARBOHYD 50 50 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 92 92 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 99 99 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 184 AA; 22072 MW; 1D051D29F979ADDE CRC64;

Query Match 37.6%; Score 328.5; DB 1; Length 184;
Best Local Similarity 45.2%; Pred. No. 1.3e-20;
Matches 75; Conservative 23; Mismatches 65; Indels 3; Gaps 2;

QY 1 MSYNLLGFLORSSNFQCKLLWQNGRLVLEYCLKDRMNFDPPEIKQLQNFSKEDAAITLY 60
DB 22 IDYKQLQFROSTSTRTCKLLRQNGRLN--LSYRTDFKIPMEVHPSQMEKSYTAFAIQ 79
QY 61 EMLQNIFAIFROSSSTGWNTEIVENLLANVYHQINHLKTVLEKLEKEDFTGRKLMSSL 120
DB 80 VMLQNVLFVRSNFSSTGWNTEIVESLLDELHQTELEILKEK-QEERLTWTSTTTL 138
QY 121 HLKRYGRILHYLKAKESYHCAMTIVRVEILRNRYFNINRLTYGLRN 166
DB 139 GLKSYVRVQRYLKKKYSYANWVVAEVRNFSIILRLNRNQ 184

RESULT 9
ID INO2_HORSE STANDARD; PRT; 195 AA.
AC P05002;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE Interferon omega-2 precursor (Interferon alpha-II-2).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP MEDLINE=87053170; PubMed=3022999;
RX Himmler A., Hauptmann R., Adolf G.R., Swetly P.;
RT "Molecular cloning and expression in Escherichia coli of equine type
RT I interferons.";
RL DNA 5:345-356(1986).
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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DR EMBL; M14545; AAA30949.1; -.
DR EMBL; A16557; CAA01293.1; -.
DR PIR; F24912; IVH022.
DR HSSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Cytokine; Glycoprotein; Antiviral; Multigene family; Signal.
FT SIGNAL 1 23
FT CHAIN 24 195 INTERFERON OMEGA-2.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
FT CARBOHYD 101 101 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 195 AA; 22131 MW; 949DA221AB3C17DF CRC64;

Query Match 32.5%; Score 284; DB 1; Length 195;
Best Local Similarity 36.6%; Pred. No. 6.8e-17;
Matches 60; Conservative 33; Mismatches 57; Indels 14; Gaps 1;

QY 2 SYNLLGFLORSSNFQCKLLWQNGRLVLEYCLKDRMNFDPPEIKQLQNFSKEDAAITLYE 61
DB 37 NEVLIGQMSRISS-----AICLKDRKDFRFPQDMADGRQPPEAQAAVLHE 82
QY 62 MLQNIFAIFROSSSTGWNTEIVENLLANVYHQINHLKTVLEKLEKEDFTGRKLMSSLH 121
DB 83 MLQIFSLFHTSRSSNAWNTLLDELCTGLLQLELDLDTCLQEGMEESALGTVPTLA 142
QY 122 LKRYGRILHYLKAKESYHCAMTIVRVEILRNRYFNINRLTYGLR 165
DB 143 VKRYFGRILHYLKAKESYHCAMTIVRVEILRNRYFNINRLTYGLR 186

RESULT 10
ID INO2_HORSE STANDARD; PRT; 195 AA.
AC P05001;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-APR-1988 (Rel. 07, Last annotation update)
DE Interferon omega-1 precursor (Interferon alpha-II-1).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP MEDLINE=87053170; PubMed=3022999;
RX Himmler A., Hauptmann R., Adolf G.R., Swetly P.;
RT "Molecular cloning and expression in Escherichia coli of equine type
RT I interferons.";
RL DNA 5:345-356(1986).
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M14544; AAA30955.1; -.
DR EMBL; A15991; CAA01259.1; -.
DR PIR; E24912; IVH021.
DR HSSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.

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Query Match      29.4%: Score 257; DB 1; Length 184;
Best Local Similarity 36.0%: Pred. No. 1.1e-14;
Matches 54; Conservative 28; Mismatches 54; Indels 14; Gaps 1;

QY 5 LLGLFQRSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEIKQLQNFskEDAALTIYEMLQ 64
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 40 LLGQRRISPPS-----CLKDRNDGFPQVEVDGQFRKQPAISAVHETIQ 85
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 65 NIFAIFRODSSSTGWNETIVENLLANVYHQINHLTKLVLEEKLEKEDTRFKLMSSHLKR 124
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 86 QIFHLFSTDGSSAAWDESLLDKLVTGLYQOOLTEELACLQSQGVGVEETPLMNEDSLAVRR 145
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 125 YYGRILHYLKAKKEYSHCAWTIVRVIELRNF 154
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 146 YFQRIALYLQEBKYSKPCAWEIVRAEIMRSF 175
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
INAA_HORSE
ID INAA_HORSE STANDARD; PRT; 184 AA.
AC P05006;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Interferon alpha-4 precursor.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053170; PubMed=3022999;
RA Hämmler A., Hauptmann R., Adolf G.R., Swetly P.;
RT "Molecular cloning and expression in Escherichia coli of equine type
RT I interferon."
RL DNA 5:345-356(1986).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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-----
CC EMBL; M14543; AAA30952.1;
CC PIR; D24912; IVHOA4.
CC HSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Cytokine; Antiviral; Multigene family; Signal.
FT SIGNAL 1 23
FT CHAIN 24 184 INTERFERON ALPHA-4.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
SQ SEQUENCE 184 AA; 20860 MW; FC087F46FLIC68EC CRC64;

Query Match      29.4%: Score 257; DB 1; Length 184;
Best Local Similarity 36.0%: Pred. No. 1.1e-14;
Matches 54; Conservative 28; Mismatches 54; Indels 14; Gaps 1;

QY 5 LLGLFQRSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEIKQLQNFskEDAALTIYEMLQ 64

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CC -----
CC EMBL; AJ000638; CAA04193.1; -.
CC HSSP; P01563; 2HIE.
CC InterPro: IPR000471; Interferon_abd.
CC Pfam; PF00143; Interferon; 1.
CC PRINTS; PR00266; INTERFERONAB.
CC ProDom; PD000550; Interferon_abd; 1.
CC SMART; SM00076; IFabd; 1.
CC pregnancy; Cytokine; Hormone; Antiviral; Signal.
KW SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 195 INTERFERON TAU.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
SQ SEQUENCE 195 AA; 22075 MW; F5304ACB1ACFOCC7 CRC64;

Query Match 29.2%; Score 255.5; DB 1; Length 195;
Best Local Similarity 37.6%; Pred. No. 1.5e-14;
Matches 56; Conservative 33; Mismatches 57; Indels 3; Gaps 2;

QY 19 KLLWLQNGRL--EYCLKDRMNFDPPEIKQLQNFSEDAALTIYEMLONFAIFRODSSS 76
DB 39 LLLGQMT-RLSPRFCLQDRKDFGLPQEMVEGGQLQDQAISVLHMLQCCFNLFHTERS 97
QY 77 TGNWETIVENLLANYVQHINHLKTVLEEKLEKEDFTRGKLMSSHLKRYVGRILHYLKAK 136
DB 98 AAWDTTLEQLTGTHQQLDDDACLGQVQMGKEDSLRMGPTLTGVKKYFGQIHVYLQEK 157
QY 137 EYSHCAWTVRVEILRNFFINRLTGCLR 165
DB 158 EYSDCAWEIVQVEMRMALSSISRLQKRLR 186

RESULT 15
ID INA2_HORSE STANDARD; PRT; 184 AA.
AC P05004;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Interferon alpha-2 precursor.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053170; PubMed=3022999;
RA HJmmler A., Hauptmann R., Adolf G.R., Swetly P.;
RT "Molecular cloning and expression in Escherichia coli of equine type
RT I interferons."
RL DNA 5:345-356(1986).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES, INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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CC -----
CC EMBL; M14541; AAA30950.1; -.
CC EMBL; A15987; CAA01258.1; -.
CC PIR; B24912; IVHOA2.
CC HSSP; P01563; 2HIE.
CC InterPro: IPR000471; Interferon_abd.
CC Pfam; PF00143; Interferon; 1.
CC PRINTS; PR00266; INTERFERONAB.
CC ProDom; PD000550; Interferon_abd; 1.
CC SMART; SM00076; IFabd; 1.
CC pregnancy; Cytokine; Hormone; Antiviral; Signal.
KW SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 184 INTERFERON ALPHA-2.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
SQ SEQUENCE 184 AA; 20877 MW; FC15DC7D811C68EC CRC64;

Query Match 28.9%; Score 253; DB 1; Length 184;
Best Local Similarity 36.0%; Pred. No. 2.3e-14;
Matches 54; Conservative 27; Mismatches 55; Indels 14; Gaps 1;

QY 5 LLGFLQRSSNFPQCKLLWLQNGRLCYCLKDRMNFDPPEIKQLQNFSEDAALTIYEMLQ 64
DB 40 LLGQMRRIISPPS-----CLKDRNDFGFPQEVDFGQFKPKQPAISAVHETIQ 85
QY 65 NIFAIFRODSSSTGWNETIVENLLANYVQHINHLKTVLEEKLEKEDFTRGKLMSSHLKLR 124
DB 86 QIFHLFTDGSAAWDESLDLKLYTGQYQQLTELEACLSQEVGEETPLMNEDSLAVRR 145
QY 125 YGRIILHYLKAKEYSHCAWTVRVEILRN 154
DB 146 YFQRIALYLOEKYSPCAWEIVRAEIMRCF 175

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Job time: 187 sec
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